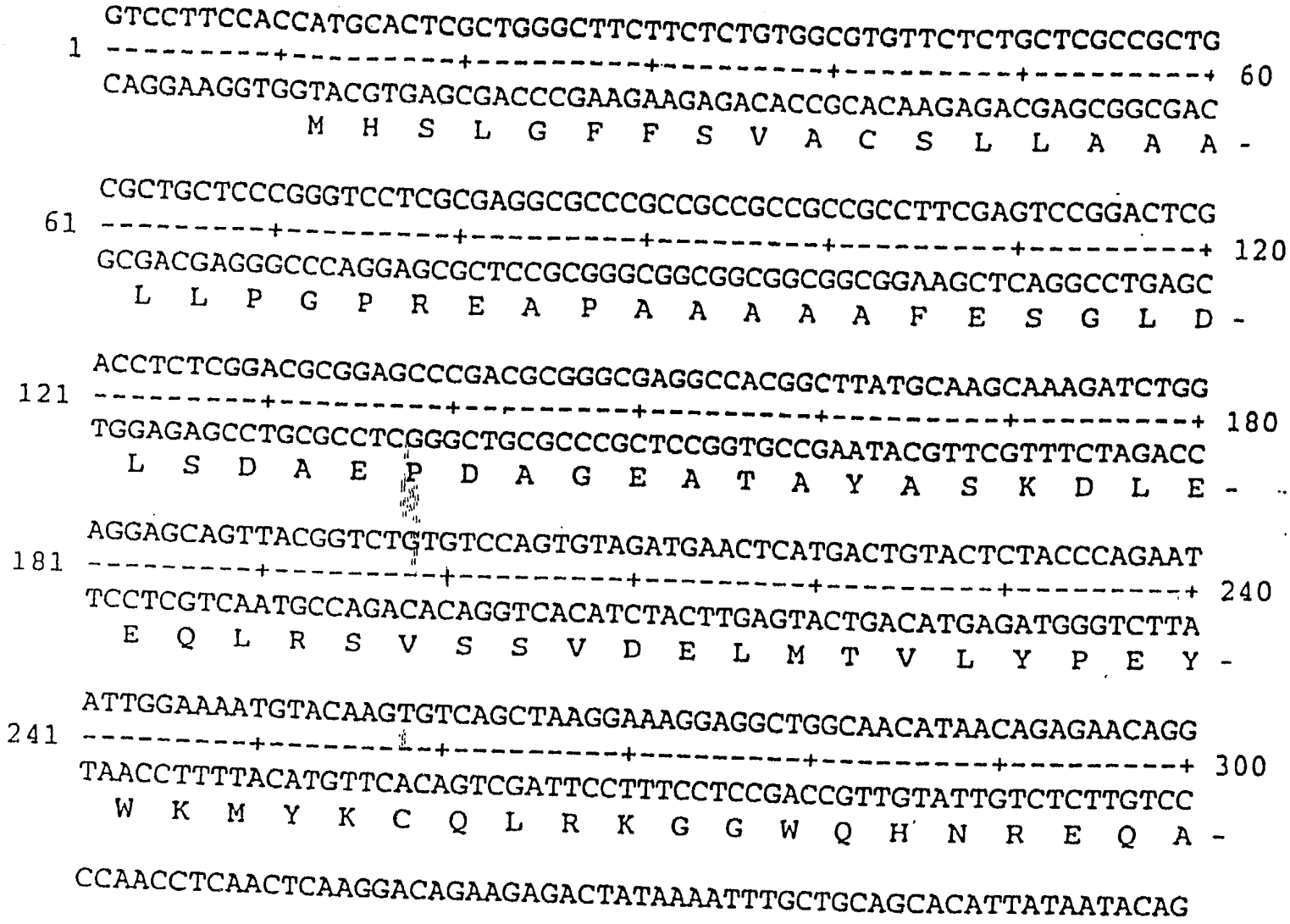


MATCH WITH FIG. 1B

FIG. 1A

MATCH WITH FIG. 1A

```
301 ---------+---------+---------+---------+---------+---------+---------+ 360
    GGTTGGAGTTGAGTTCCTGTCTTCTCTGATATTTTAAACGACGTCGTGTAATATTATGTC
      N  L  N  S  R  T  E  E  T  I  K  F  A  A  A  H  Y  N  T  E -

    AGATCTTGAAAAGTATTGATAATGAGTGGAGAAAGACTCAATGCATGCCACGGGAGGTGT
361 ---------+---------+---------+---------+---------+---------+---------+ 420
    TCTAGAACTTTTCATAACTATTACTCACCTCTTTCTGAGTTACGTACGGTGCCCTCCACA
      I  L  K  S  I  D  N  E  W  R  K  T  Q  C  M  P  R  E  V  C -

    GTATAGATGTGGGGAAGGAGTTTGGAGTCGCGACAAACACCTTCTTTAAACCTCCATGTG
421 ---------+---------+---------+---------+---------+---------+---------+ 480
    CATATCTACACCCCTTCCTCAAACCTCAGCGCTGTTTGTGGAAGAAATTTGGAGGTACAC
      I  D  V  G  K  E  F  G  V  A  T  N  T  F  F  K  P  P  C  V -

    TGTCCGTCTACAGATGTGGGGGTTGCTGCAATAGTGAGGGGCTGCAGTGCATGAACACCA
481 ---------+---------+---------+---------+---------+---------+---------+ 540
    ACAGGCAGATGTCTACACCCCCAACGACGTTATCACTCCCCGACGTCACGTACTTGTGGT
      S  V  Y  R  C  G  G  C  C  N  S  E  G  L  Q  C  M  N  T  S -

    GCACGAGCTACCTCAGCAAGACGTTATTTGAAATTACAGTGCCTCTCTCTCAAGGCCCCA
541 ---------+---------+---------+---------+---------+---------+---------+ 600
    CGTGCTCGATGGAGTCGTTCTGCAATAAACTTTAATGTCACGGAGAGAGAGTTCCGGGGT
      T  S  Y  L  S  K  T  L  F  E  I  T  V  P  L  S  Q  G  P  K -

    AACCAGTAACAATCAGTTTTGCCAATCACACTTCCTGCCGATGCATGTCTAAACTGGATG
601 ---------+---------+---------+---------+---------+---------+---------+ 660
    TTGGTCATTGTTAGTCAAAACGGTTAGTGTGAAGGACGGCTACGTACAGATTTGACCTAC
      P  V  T  I  S  F  A  N  H  T  S  C  R  C  M  S  K  L  D  V -
```

MATCH WITH FIG. 1C

FIG. 1B

MATCH WITH FIG. 1B

```
    TTTACAGACAAGTTCATTCCATTATTAGACGTTCCCTGCCAGCAACACTACCACAGTGTC
661 ---------+---------+---------+---------+---------+---------+ 720
    AAATGTCTGTTCAAGTAAGGTAATAATCTGCAAGGGACGGTCGTTGTGATGGTGTCACAG
      Y  R  Q  V  H  S  I  I  R  R  S  L  P  A  T  L  P  Q  C  Q -

    AGGCAGCGAACAAGACCTGCCCCACCAATTACATGTGGAATAATCACATCTGCAGATGCC
721 ---------+---------+---------+---------+---------+---------+ 780
    TCCGTCGCTTGTTCTGGACGGGGTGGTTAATGTACACCTTATTAGTGTAGACGTCTACGG
      A  A  N  K  T  C  P  T  N  Y  M  W  N  N  H  I  C  R  C  L -

    TGGCTCAGGAAGATTTTATGTTTTCCTCGGATGCTGGAGATGACTCAACAGATGGATTCC
781 ---------+---------+---------+---------+---------+---------+ 840
    ACCGAGTCCTTCTAAAATACAAAAGGAGCCTACGACCTCTACTGAGTTGTCTACCTAAGG
      A  Q  E  D  F  M  F  S  S  D  A  G  D  D  S  T  D  G  F  H -

    ATGACATCTGTGGACCAAACAAGGAGCTGGATGAAGAGACCTGTCAGTGTGTCTGCAGAG
841 ---------+---------+---------+---------+---------+---------+ 900
    TACTGTAGACACCTGGTTTGTTCCTCGACCTACTTCTCTGGACAGTCACACAGACGTCTC
      D  I  C  G  P  N  K  E  L  D  E  E  T  C  Q  C  V  C  R  A -

    CGGGGCTTCGGCCTGCCAGCTGTGGACCCCACAAAGAACTAGACAGAAACTCATGCCAGT
901 ---------+---------+---------+---------+---------+---------+ 960
    GCCCCGAAGCCGGACGGTCGACACCTGGGGTGTTTCTTGATCTGTCTTTGAGTACGGTCA
      G  L  R  P  A  S  C  G  P  H  K  E  L  D  R  N  S  C  Q  C -

    GTGTCTGTAAAAACAAACTCTTCCCCAGCCAATGTGGGGCCAACCGAGAATTTGATGAAA
961 ---------+---------+---------+---------+---------+---------+ 1020
    CACAGACATTTTTGTTTGAGAAGGGGTCGGTTACACCCCGGTTGGCTCTTAAACTACTTT
```

MATCH WITH FIG. 1D

FIG. 1C

MATCH WITH FIG. 1C

```
      V  C  K  N  K  L  F  P  S  Q  C  G  A  N  R  E  F  D  E  N -

      ACACATGCCAGTGTGTATGTAAAAGAACCTGCCCCAGAAATCAACCCCTAAATCCTGGAA
1021  ---------+---------+---------+---------+---------+---------+---------+ 1080
      TGTGTACGGTCACACATACATTTTCTTGGACGGGGTCTTTAGTTGGGGATTTAGGACCTT
        T  C  Q  C  V  C  K  R  T  C  P  R  N  Q  P  L  N  P  G  K -

      AATGTGCCTGTGAATGTACAGAAAGTCCACAGAAATGCTTGTTAAAAGGAAAGAAGTTCC
1081  ---------+---------+---------+---------+---------+---------+---------+ 1140
      TTACACGGACACTTACATGTCTTTCAGGTGTCTTTACGAACAATTTTCCTTTCTTCAAGG
        C  A  C  E  C  T  E  S  P  Q  K  C  L  L  K  G  K  K  F  H -

      ACCACCAAACATGCAGCTGTTACAGACGGCCATGTACGAACCGCCAGAAGGCTTGTGAGC
1141  ---------+---------+---------+---------+---------+---------+---------+ 1200
      TGGTGGTTTGTACGTCGACAATGTCTGCCGGTACATGCTTGGCGGTCTTCCGAACACTCG
        H  Q  T  C  S  C  Y  R  R  P  C  T  N  R  Q  K  A  C  E  P -

      CAGGATTTTCATATAGTGAAGAAGTGTGTCGTTGTGTCCCTTCATATTGGCAAAGACCAC
1201  ---------+---------+---------+---------+---------+---------+---------+ 1260
      GTCCTAAAAGTATATCACTTCTTCACACAGCAACACAGGGAAGTATAACCGTTTCTGGTG
        G  F  S  Y  S  E  E  V  C  R  C  V  P  S  Y  W  Q  R  P  Q -

      AAATGAGCTAAGATTGTACTGTTTTCCAGTTCATCGATTTTCTATTATGGAAAACTGTGT
```

MATCH WITH FIG. 1E

FIG. 1D

MATCH WITH FIG. 1D

```
1261 ---------+---------+---------+---------+---------+---------+ 1320
     TTTACTCGATTCTAACATGACAAAAGGTCAAGTAGCTAAAAGATAATACCTTTTGACACA
       M   S   *

     TGCCACAGTAGAACTGTCTGTGAACAGAGAGACCCTTGTGGGTCCATGCTAACAAAGACA
1321 ---------+---------+---------+---------+---------+---------+ 1380
     ACGGTGTCATCTTGACAGACACTTGTCTCTCTGGGAACACCCAGGTACGATTGTTTCTGT

     AAAGTCTGTCTTTCCTGAACCATGTGGATAACTTTACAGAAATGGACTGGAGCTCATCTG
1381 ---------+---------+---------+---------+---------+---------+ 1440
     TTTCAGACAGAAAGGACTTGGTACACCTATTGAAATGTCTTTACCTGACCTCGAGTAGAC

     CAAAAGGCCTCTTGTAAAGACTGGTTTTCTGCCAATGACCAAACAGCCAAGATTTTCCTC
1441 ---------+---------+---------+---------+---------+---------+ 1500
     GTTTTCCGGAGAACATTTCTGACCAAAAGACGGTTACTGGTTTGTCGGTTCTAAAAGGAG

     TTGTGATTTCTTTAAAAGAATGACTATATAATTTATTTCCACTAAAAATATTGTTTCTGC
1501 ---------+---------+---------+---------+---------+---------+ 1560
     AACACTAAAGAAATTTTCTTACTGATATATTAAATAAAGGTGATTTTTATAACAAAGACG

     ATTCATTTTTATAGCAACAACAATTGGTAAAACTCACTGTGATCAATATTTTTATATCAT
1561 ---------+---------+---------+---------+---------+---------+ 1620
     TAAGTAAAAATATCGTTGTTGTTAACCATTTTGAGTGACACTAGTTATAAAAATATAGTA

     GCAAAATATGTTTAAAATAAAATGAAAATTGTATTTATAAAAAAAAAAAAAAAA
1621 ---------+---------+---------+---------+---------+----  1674
     CGTTTTATACAAATTTTATTTTACTTTTAACATAAATATTTTTTTTTTTTTTTT
```

FIG. 1E

```
   1  CGAGGCCACGGCTTATGCAAGCAAAGATCTGGAGGAGCAGTTACGGTCTGTGTCCAGTGT
      ---------+---------+---------+---------+---------+---------+
                M  T  V  L  Y  P  E  Y  W  K  M  Y  K  C  Q  L  R

  71  AGATGAACTCATGACTGTACTCTACCCAGAATATTGGAAAATGTACAAGTGTCAGCTAAG
      ---------+---------+---------+---------+---------+---------+
       K  G  G  W  Q  H  N  R  E  Q  A  N  L  N  S  R  T  E  E  T

 121  GAAAGGAGGCTGGCAACATAACAGAGAACAGGCCAACCTCAACTCAAGGACAGAAGAGAC
      ---------+---------+---------+---------+---------+---------+
       I  K  F  A  A  A  H  Y  N  T  E  I  L  K  S  I  D  N  E  W

 181  TATAAAATTTGCTGCAGCACATTATAATACAGAGATCTTGAAAAGTATTGATAATGAGTG
      ---------+---------+---------+---------+---------+---------+
       R  K  T  Q  C  M  P  R  E  V  C  I  D  V  G  K  E  F  G  V

 241  GAGAAAGACTCAATGCATGCCACGGGAGGTGTGTATAGATGTGGGGAAGGAGTTTGGAGT
      ---------+---------+---------+---------+---------+---------+
       A  T  N  T  F  F  K  P  P  C  V  S  V  Y  R  C  G  G  C  C

 301  CGCGACAAACACCTTCTTTAAACCTCCATGTGTGTCCGTCTACAGATGTGGGGGTTGCTG
      ---------+---------+---------+---------+---------+---------+
```

FIG. 2A

```
361  CAATAGTGAGGGGCTGCAGTGCATGAACACCAGCACGAGCTACCTCAGCAAGACGTTATT
     ---------+---------+---------+---------+---------+---------+---------+
      N  S  E  G  L  Q  C  M  N  T  S  T  S  Y  L  S  K  T  L  F

421  TGAAATTACAGTGCCTCTCTCTCAAGGCCCCAAACCAGTAACAATCAGTTTTGCCAATCA
     ---------+---------+---------+---------+---------+---------+---------+
      E  I  T  V  P  L  S  Q  G  P  K  P  V  T  I  S  F  A  N  H

481  CACTTCCTGCCGATGCATGTCTAAACTGGATGTTTACAGACAAGTTCATTCCATTATTAG
     ---------+---------+---------+---------+---------+---------+---------+
      T  S  C  R  C  M  S  K  L  D  V  Y  R  Q  V  H  S  I  I  R

541  ACGTTCCCTGCCAGCAACACTACCACAGTGTCAGGCAGCGAACAAGACCTGCCCCACCAA
     ---------+---------+---------+---------+---------+---------+---------+
      R  S  L  P  A  T  L  P  Q  C  Q  A  A  N  K  T  C  P  T  N

601  TTACATGTGGAATAATCACATCTGCAGATGCCTGGCTCAGGAAGATTTTATGTTTTCCTC
     ---------+---------+---------+---------+---------+---------+---------+
      Y  M  W  N  N  H  I  C  R  C  L  A  Q  E  D  F  M  F  S  S

661  GGATGCTGGAGATGACTCAACAGATGGATTCCATGACATCTGTGGACCAAACAAGGAGCT
     ---------+---------+---------+---------+---------+---------+---------+
      D  A  G  D  D  S  T  D  G  F  H  D  I  C  G  P  N  K  E  L
```

FIG. 2B

```
721  GGATGAAGAGACCTGTCAGTGTGTCTGCAGAGCGGGGCTTCGGCCTGCCAGCTGTGGACC
     ---------+---------+---------+---------+---------+---------+
      D  E  E  T  C  Q  C  V  C  R  A  G  L  R  P  A  S  C  G  P

781  CCACAAAGAACTAGACAGAAACTCATGCCAGTGTGTCTGTAAAAACAAACTCTTCCCCAG
     ---------+---------+---------+---------+---------+---------+
      H  K  E  L  D  R  N  S  C  Q  C  V  C  K  N  K  L  F  P  S

841  CCAATGTGGGGCCAACCGAGAATTTGATGAAAACACATGCCAGTGTGTATGTAAAAGAAC
     ---------+---------+---------+---------+---------+---------+
      Q  C  G  A  N  R  E  F  D  E  N  T  C  Q  C  V  C  K  R  T

901  CTGCCCCAGAAATCAACCCCTAAATCCTGGAAAATGTGCCTGTGAATGTACAGAAAGTCC
     ---------+---------+---------+---------+---------+---------+
      C  P  R  N  Q  P  L  N  P  G  K  C  A  C  E  C  T  E  S  P

961  ACAGAAATGCTTGTTAAAAGGAAAGAAGTTCCACCACCAAACATGCAGCTGTTACAGACG
     ---------+---------+---------+---------+---------+---------+
      Q  K  C  L  L  K  G  K  K  F  H  H  Q  T  C  S  C  Y  R  R

1021 GCCATGTACGAACCGCCAGAAGGCTTGTGAGCCAGGATTTTCATATAGTGAAGAAGTGTG
     ---------+---------+---------+---------+---------+---------+
      P  C  T  N  R  Q  K  A  C  E  P  G  F  S  Y  S  E  E  V  C
```

FIG. 2C

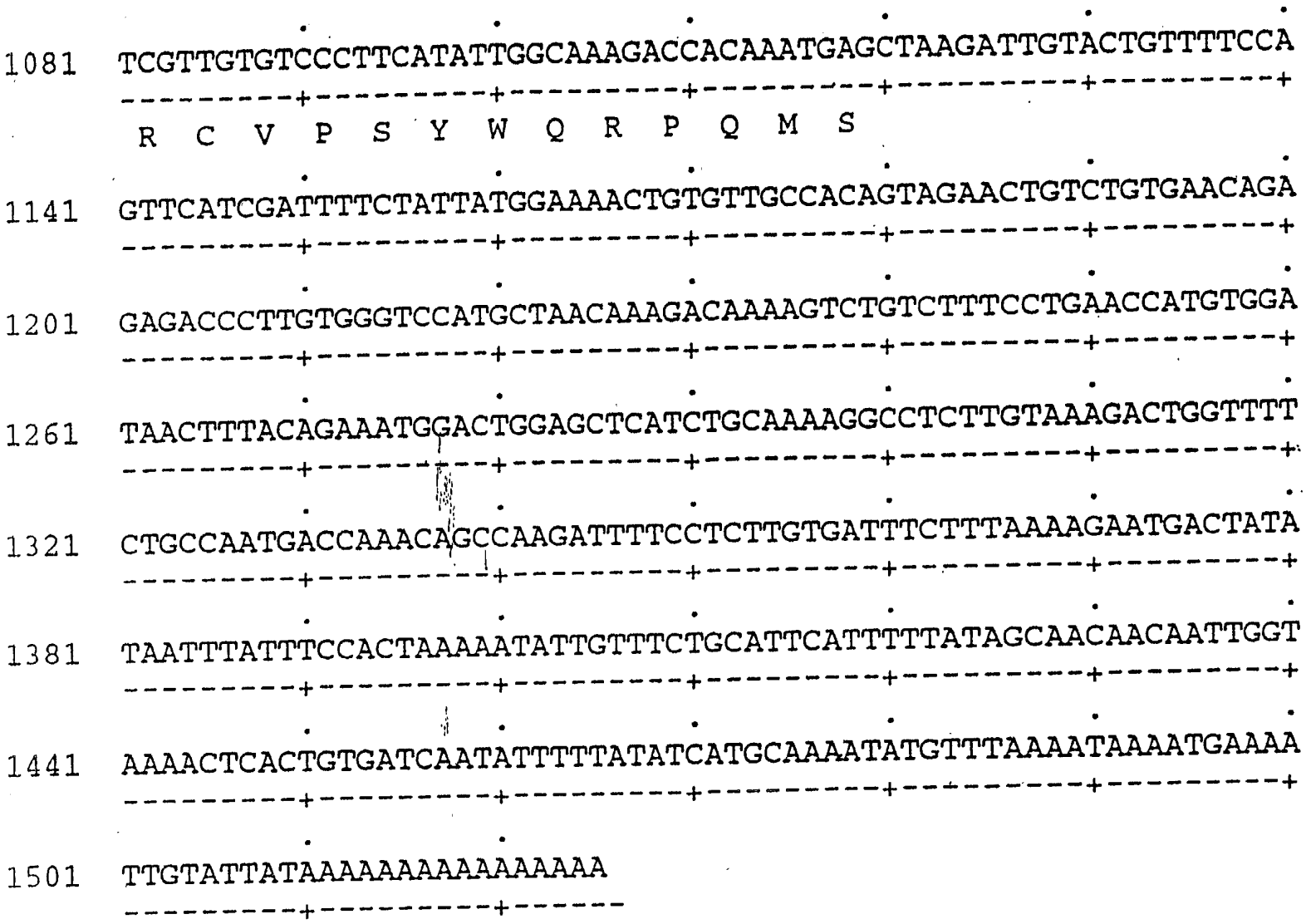


FIG. 2D

```
           1                                                    50
Pdgfa .MRTLACLLL LGCGYLAHVL AEEAEIPREV IERLARSQIH SIRDLQRLLE
Pdgfb MNRCWA.LFL SLCCYLRLVS AEGDPIPEEL YEMLSDHSIR SFDDLQRLLH
 Vegf .....MNFLL SWVHWSLALL LY........ .......... .LHHAKWSQA
Vegf2 .......MTV LYPEYWKMYK CQ........ .......... .LRKGGWQHN

      51                                                   100
Pdgfa IDSVGSEDSL DTSLRAHGVH ATKHVPEKRP LPIRRKRSI. .....EEAVP
Pdgfb GDP.GEEDGA ELDLNMTRSH SGGELES... .LARGRRSLG SLTIAEPAMI
 Vegf APMAE..... ......GGGQ NHHEVVKFMD .VYQR..... ..........
Vegf2 REQANLNSRT EETIKFAAAH YNTEILKSID NEWRK..... ..........

      101                                                  150
Pdgfa AVCKTRTVIY EIPRSQVDPT SANFLIWPPC VEVKRCTGCC NTSSVKCQPS
Pdgfb AECKTRTEVF EISRRLIDRT NANFLVWPPC VEVQRCSGCC NNRNVQCRPT
 Vegf SYCHPIETLV DIFQEYPDEI ..EYIFKPSC VPLMRCGGCC NDEGLECVPT
Vegf2 TQCMPREVCI DVGKEFGVAT ..NTFFKPPC VSVYRCGGCC NSEGLQCMNT

      151                                                  200
Pdgfa RVHHRSVKVA KVEYVRKKPK LKEVQVRLEE HLECAC.... AT........
Pdgfb QVQLRPVQVR KIEIVRKKPI FKKATVTLED HLACKC.... ETVAAARPVT
 Vegf EESNITMQIM RIK.PH..QG QHIGEMSFLQ HNKCECRPKK DRARQEKKSV
Vegf2 STSYLSKTLF EIT.VPLSQG PKPVTISFAN HTSCRCMSKL DVYRQVHSII
```

FIG. 3A

```
                                                                    250
      201
Pdgfa ....TSLNPD YREEDTDVR. ..... ..... .....
Pdgfb RSPGGSQEQR AKTPQTRVTI RTVRVRRPPK GKHRKFKHTH DKTALKETLG
 Vegf RGK..... .GKGQKRKRK KSRYKSWSVY VGARCCLMPW SLPGPHP...
Vegf2 RRSLPATLPQ CQAANKTCPT NYMWNNHICR CLAQEDFMFS SDAGDDSTDG
                                                                    300
      251
Pdgfa ..... ..... ..... ..... .....
Pdgfb A..... ..... ..... ..... .....
 Vegf ....CGP... ..... .....CSE RRKHLFVQDP QTCKCSCKNT
Vegf2 FHDICGPNKE LDEETCQCVC RAGLRPASCG PHKEL...DR NSCQCVCKNK
                                                                    350
      301
Pdgfa ..... ..... ..... ..... .....
Pdgfb ..... ..... ..... ..... .....
 Vegf ..DSRCKARQ LELNERTCRC DKPRR..... ..... .....
Vegf2 LFPSQCGANR .EFDENTCQC VCKRTCPRNQ PLNPGKCACE CTESPQKCLL
                                                                    398
      351
Pdgfa ..... ..... ..... ..... .....
Pdgfb ..... ..... ..... ..... .....
 Vegf ..... ..... ..... ..... .....
Vegf2 KGKKFHHQTC SCYRRPCTNR QKACEPGFSY SEEVCRCVPS YWQRPQMS
```

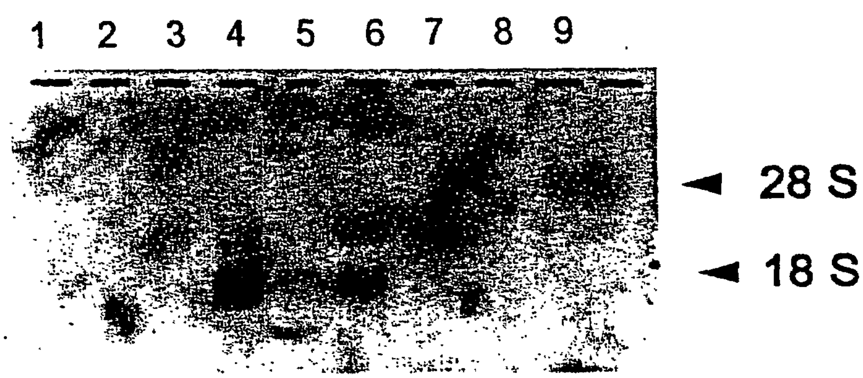
FIG. 3B

PERCENTAGE (%) OF AMINO ACID IDENTITIES BETWEEN EACH PAIR OF GENES IS SHOWN IN THE FOLLWING TABLE

	PDGFα	PDGFβ	VEGF	VEGF2
PDGFα				
PDGFβ	48.0			
VEGF	20.7	22.7		
VEGF2	23.5	22.4	30.0	

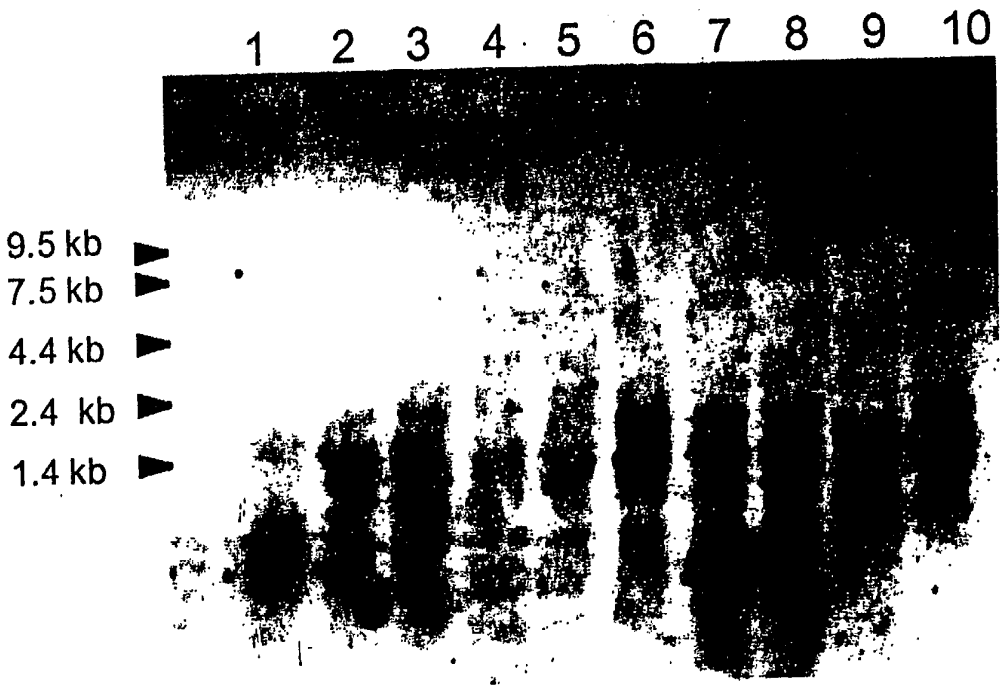
FIG.4

Expression of VEGF2 mRNA in Human Breast Tumor Cells



Lane 1. normal breast tissue
Lane 2. breast tumor tissue
Lane 3-9. breast tumor cell lines.

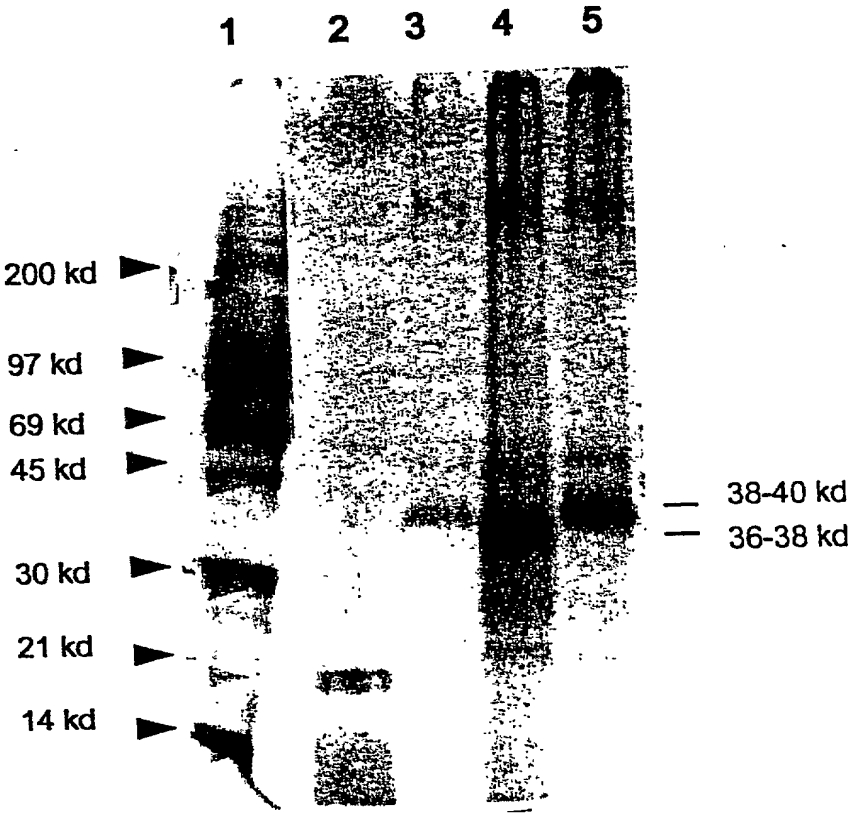
FIG.5



1.	ovary	6.	lung
2.	testes	7.	spleen
3.	gall bladder	8.	prostate
4.	kidney	9.	Hippocampus
5.	liver	10.	heart

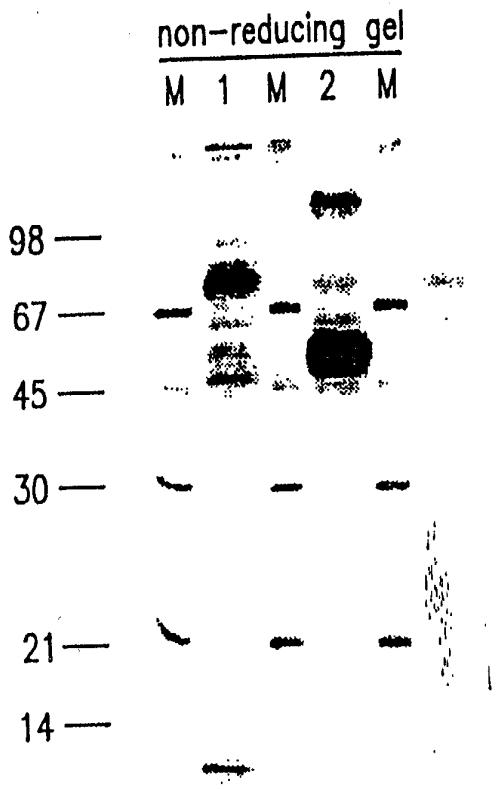
Expression of VEGF2 mRNA in human adult tissues.

FIG.6



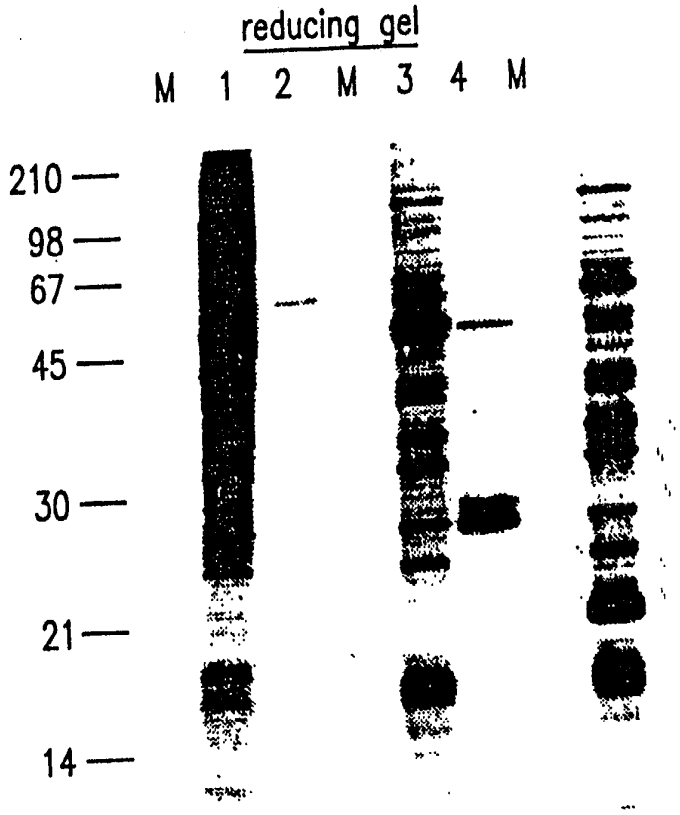
Lane 1: 14-C and rainbow M.W. marker
Lane 2: FGF control
Lane 3: VEGF2 (M13-reverse $ forward primers)
Lane 4: VEGF2 (M13-reverse & VEGF-F4 primers)
Lane 5: VEGF2 (M13-reverse & VEGF-F5 primers)

FIG.7



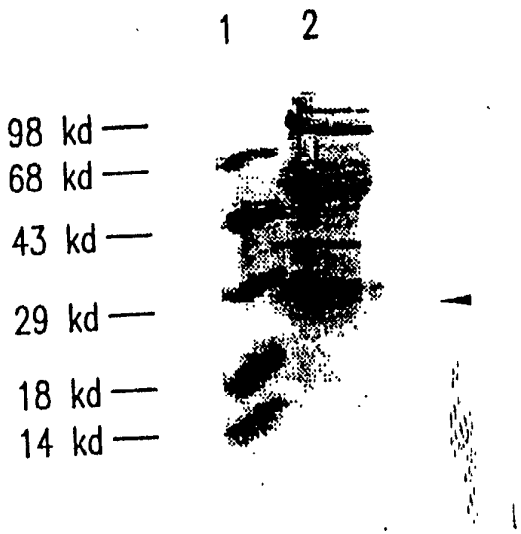
Lane M Marker
Lane 1 vector medium
Lane 2 VEGF2 medium

FIG.8A



Lane M: Marker
Lane 1: vector Cytoplasm
Lane 2: vector medium
Lane 3: VEGF2 Cytoplasm
Lane 4: VEGF2 medium

FIG.8B



Lane 1: Molelular weight marker
Lane 2: Precipitates containing VEGF2.

FIG.9

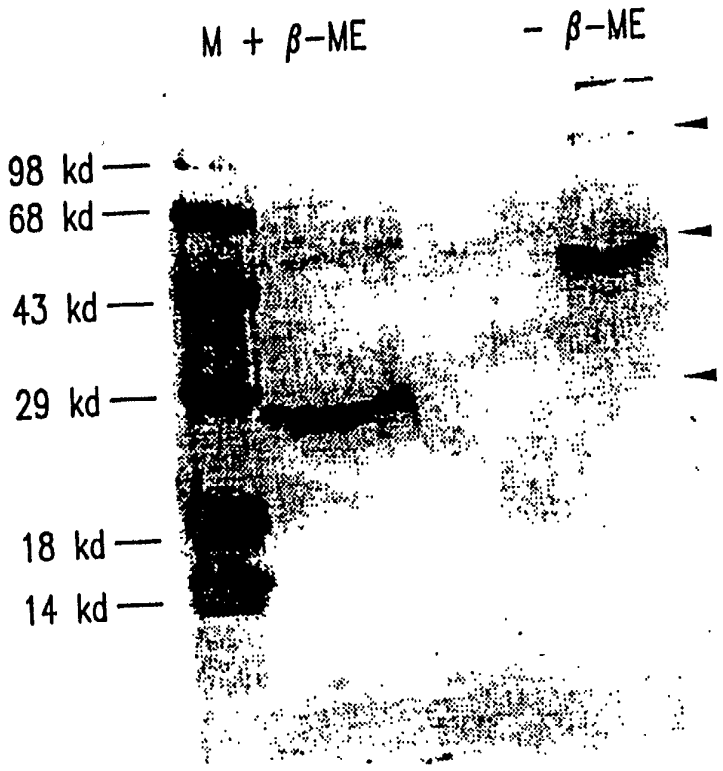


FIG.10

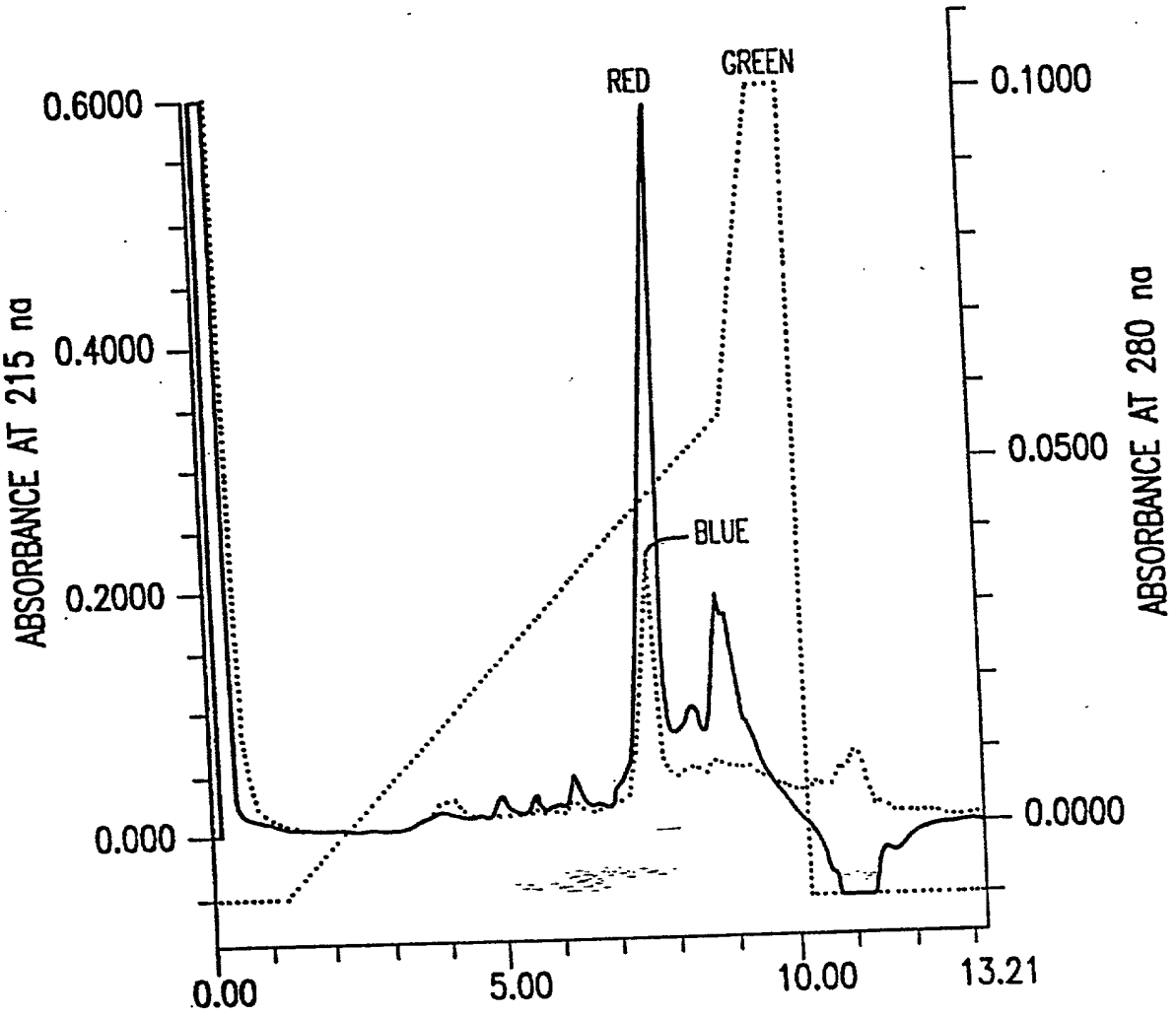

RED
GREEN
BLUE
0.6000
0.4000
0.2000
0.000
ABSORBANCE AT 215 nm
0.1000
0.0500
0.0000
ABSORBANCE AT 280 nm
0.00
5.00
10.00
13.21

FIG. 11

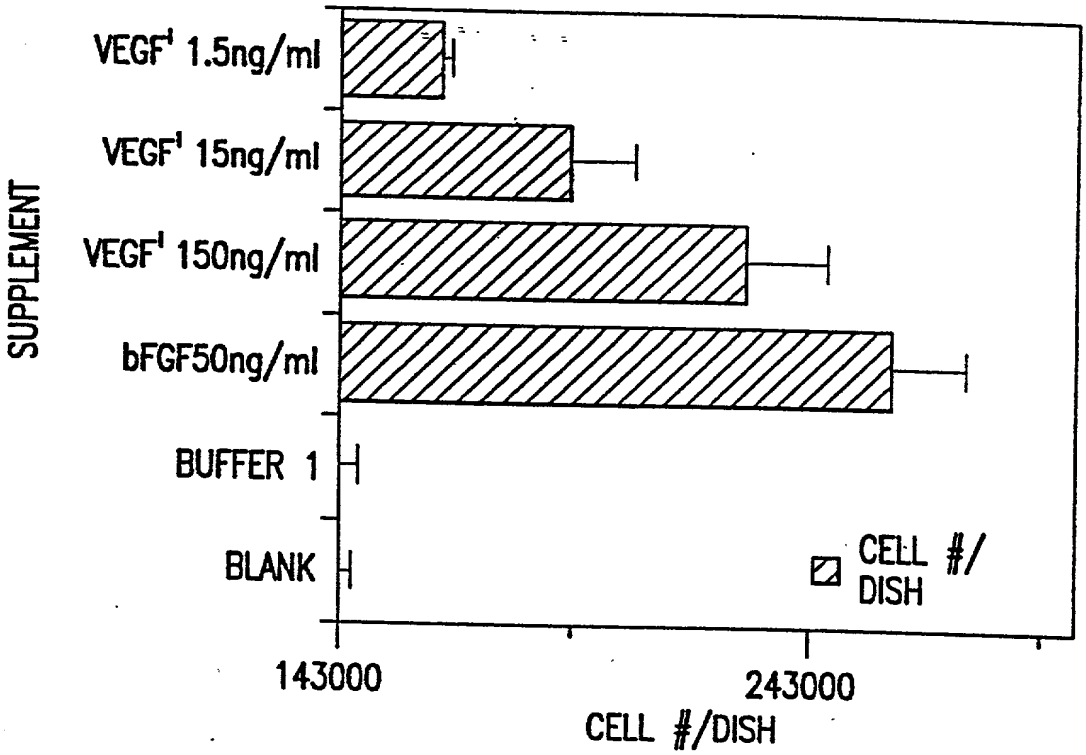

VEGF' 1.5ng/ml
VEGF' 15ng/ml
VEGF' 150ng/ml
bFGF50ng/ml
BUFFER 1
BLANK
SUPPLEMENT
CELL #/ DISH
143000
243000
CELL #/DISH

FIG.12

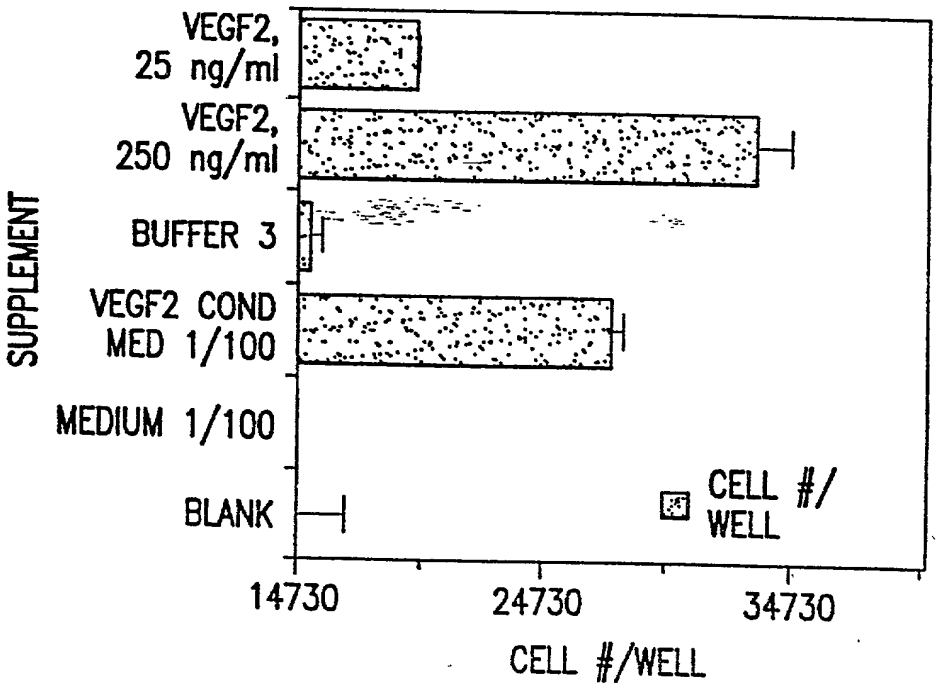

VEGF2, 25 ng/ml
VEGF2, 250 ng/ml
BUFFER 3
VEGF2 COND MED 1/100
MEDIUM 1/100
BLANK
SUPPLEMENT
CELL #/ WELL
14730
24730
34730
CELL #/WELL

FIG.13

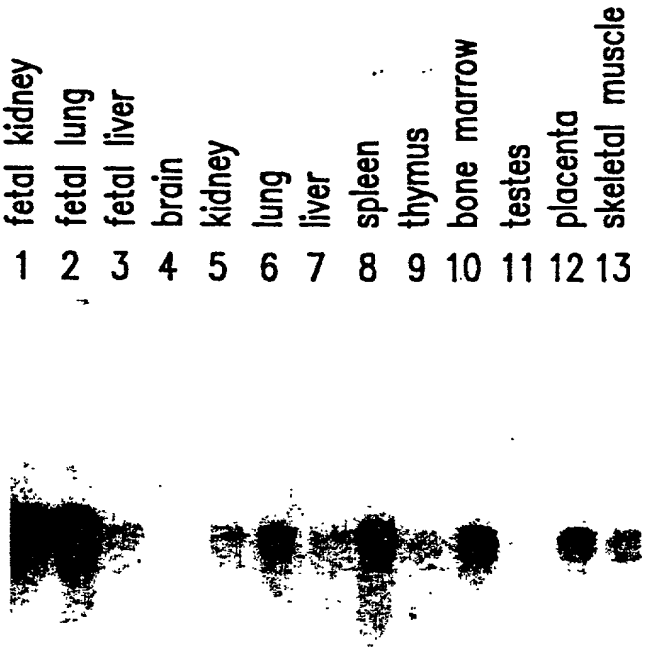
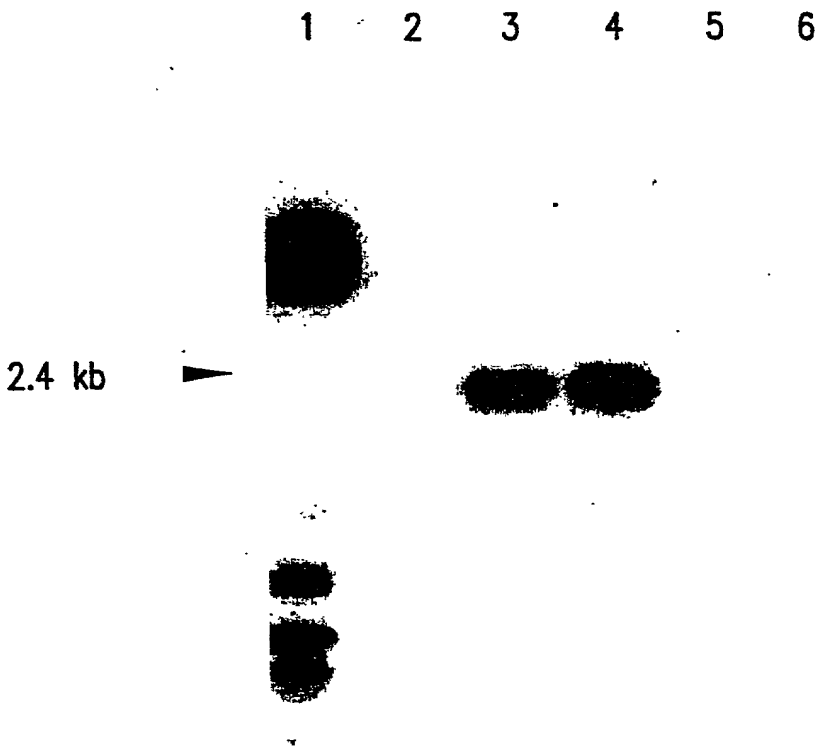


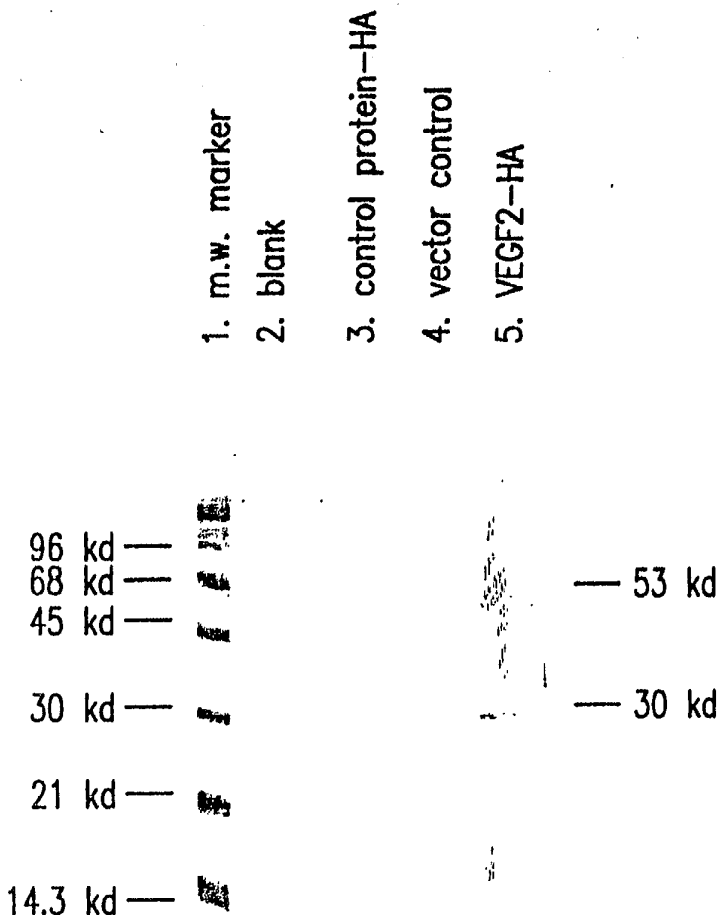
FIG.14A

FIG.14B



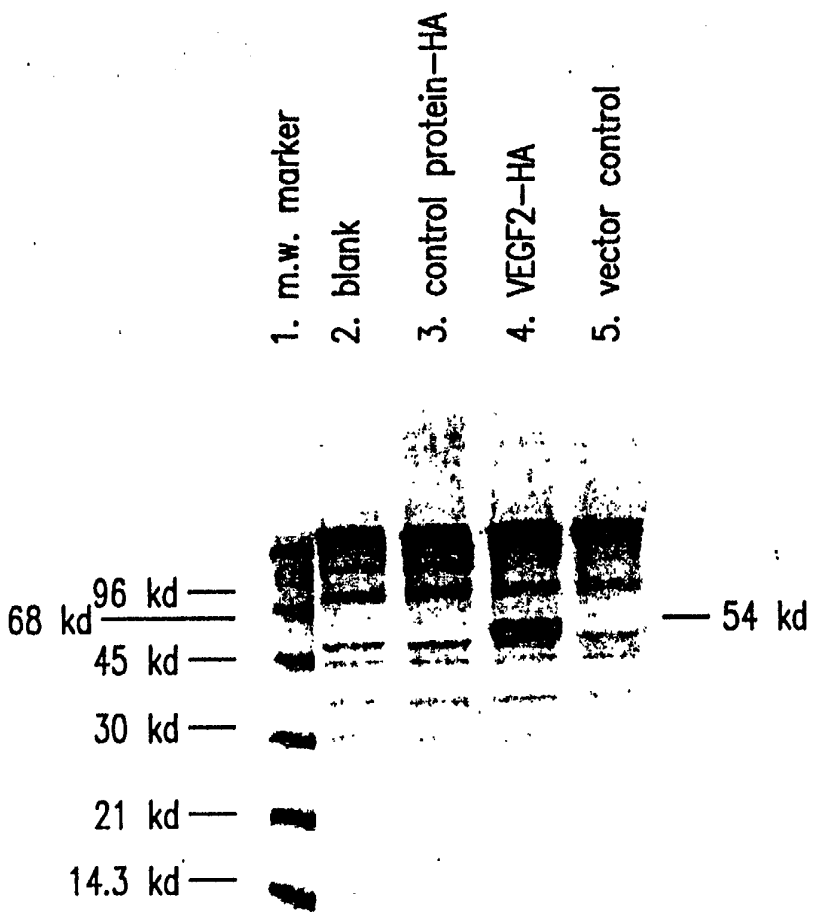
1. Molecular Weight Marker
2. umbelical vein endothelial cells
3. aortic smooth muscle cells
4. Dermal fibroblast

FIG.15



conditioned medium

FIG.16A



cell lysate

FIG.16B

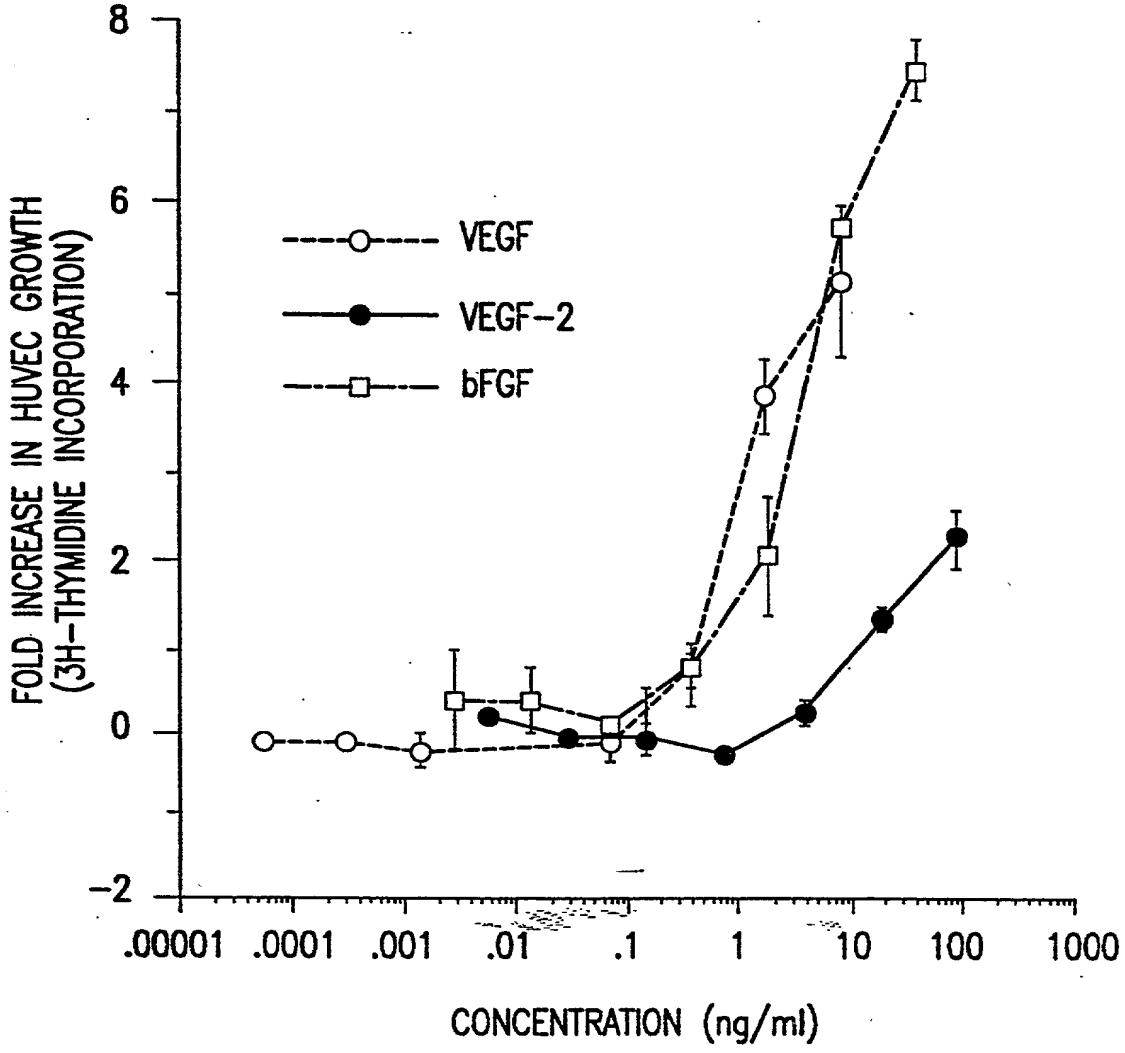

8
6
4
2
0
-2
FOLD INCREASE IN HUVEC GROWTH
(3H-THYMIDINE INCORPORATION)
VEGF
VEGF-2
bFGF
.00001
.0001
.001
.01
.1
1
10
100
1000
CONCENTRATION (ng/ml)

FIG.17

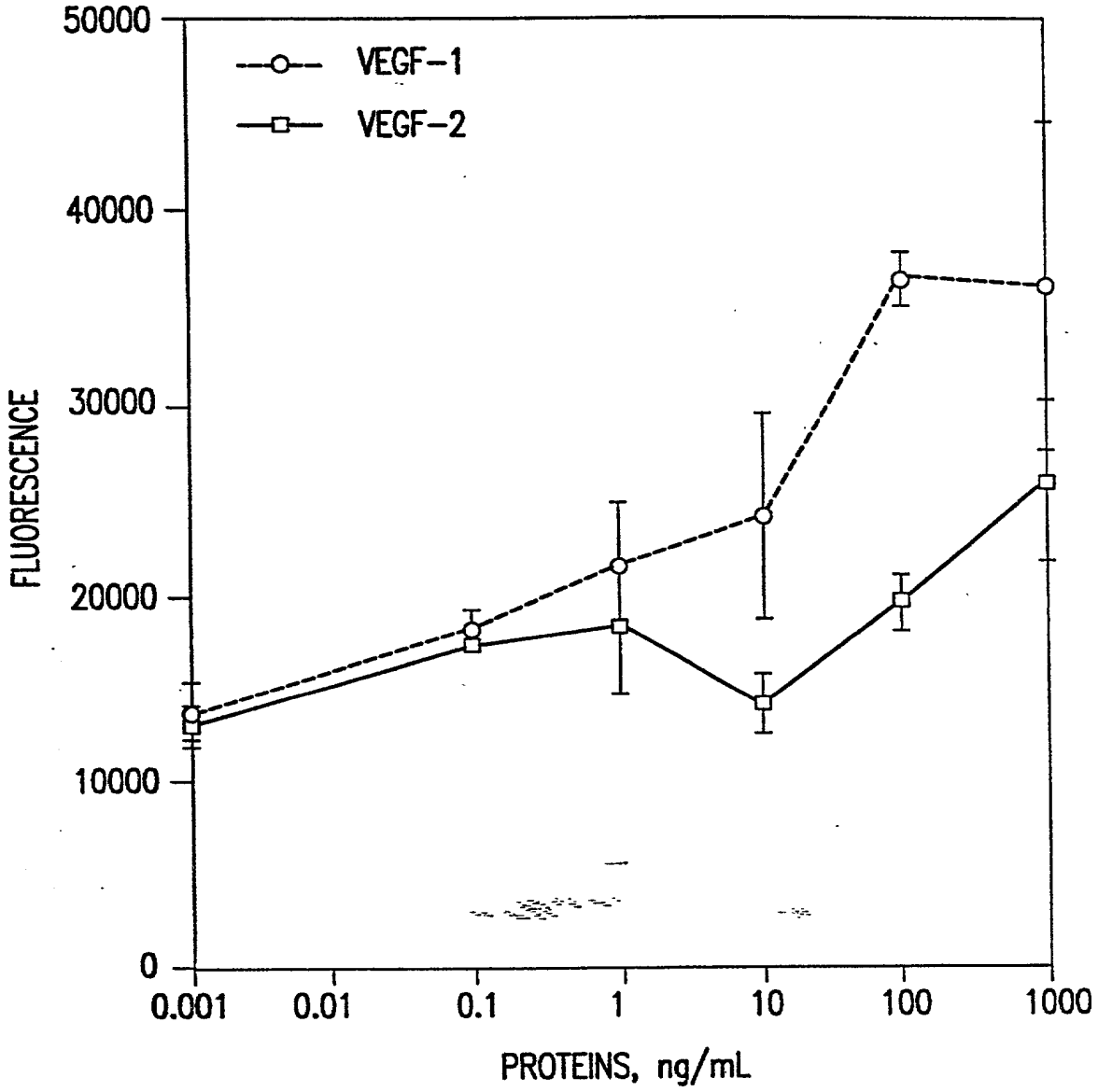

50000
40000
30000
20000
10000
0
FLUORESCENCE
VEGF-1
VEGF-2
0.001
0.01
0.1
1
10
100
1000
PROTEINS, ng/mL

FIG.18

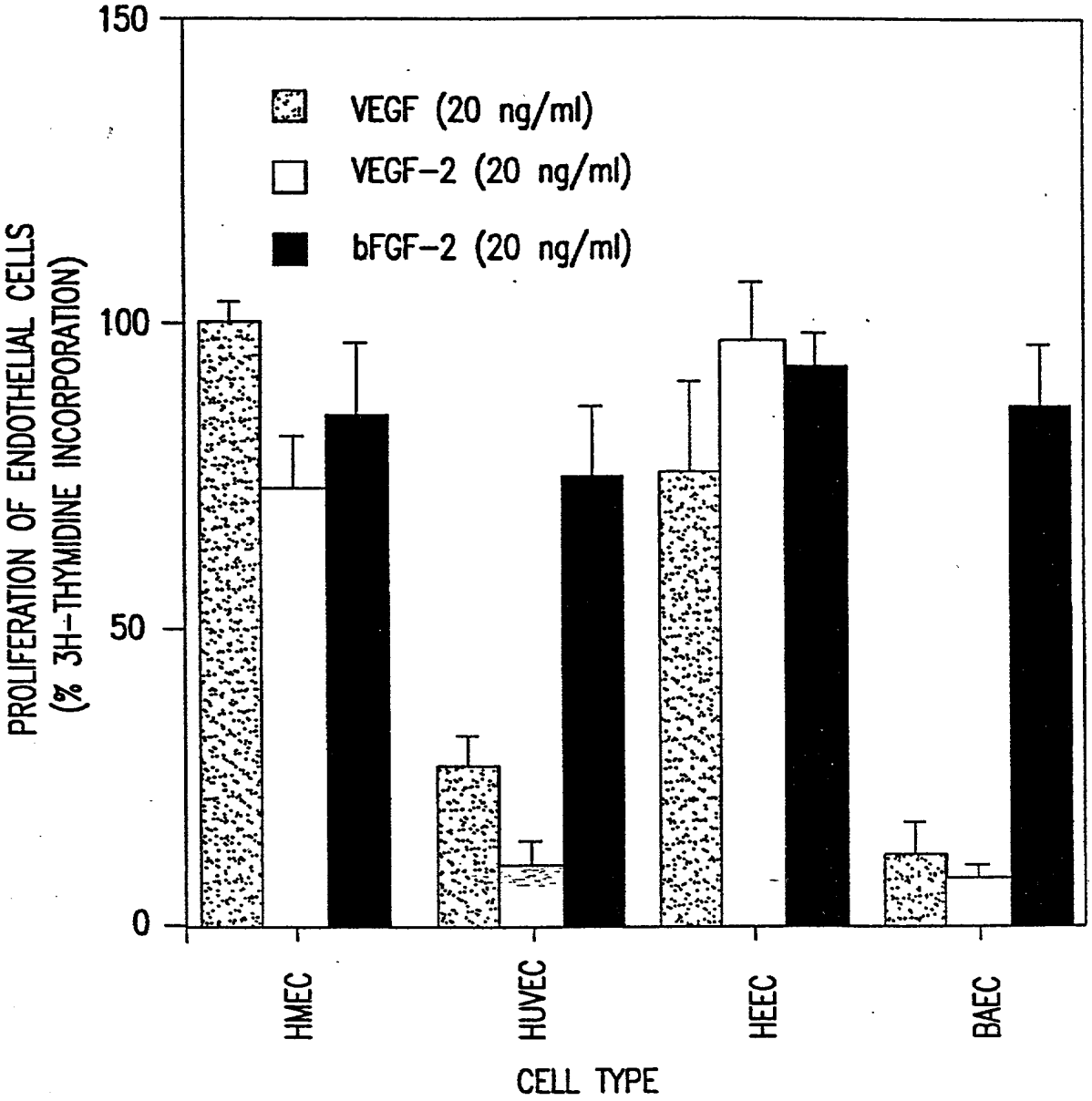

150
100
50
0
VEGF (20 ng/ml)
VEGF-2 (20 ng/ml)
bFGF-2 (20 ng/ml)
PROLIFERATION OF ENDOTHELIAL CELLS
(% 3H-THYMIDINE INCORPORATION)
HMEC
HUVEC
HEEC
BAEC
CELL TYPE

FIG.19

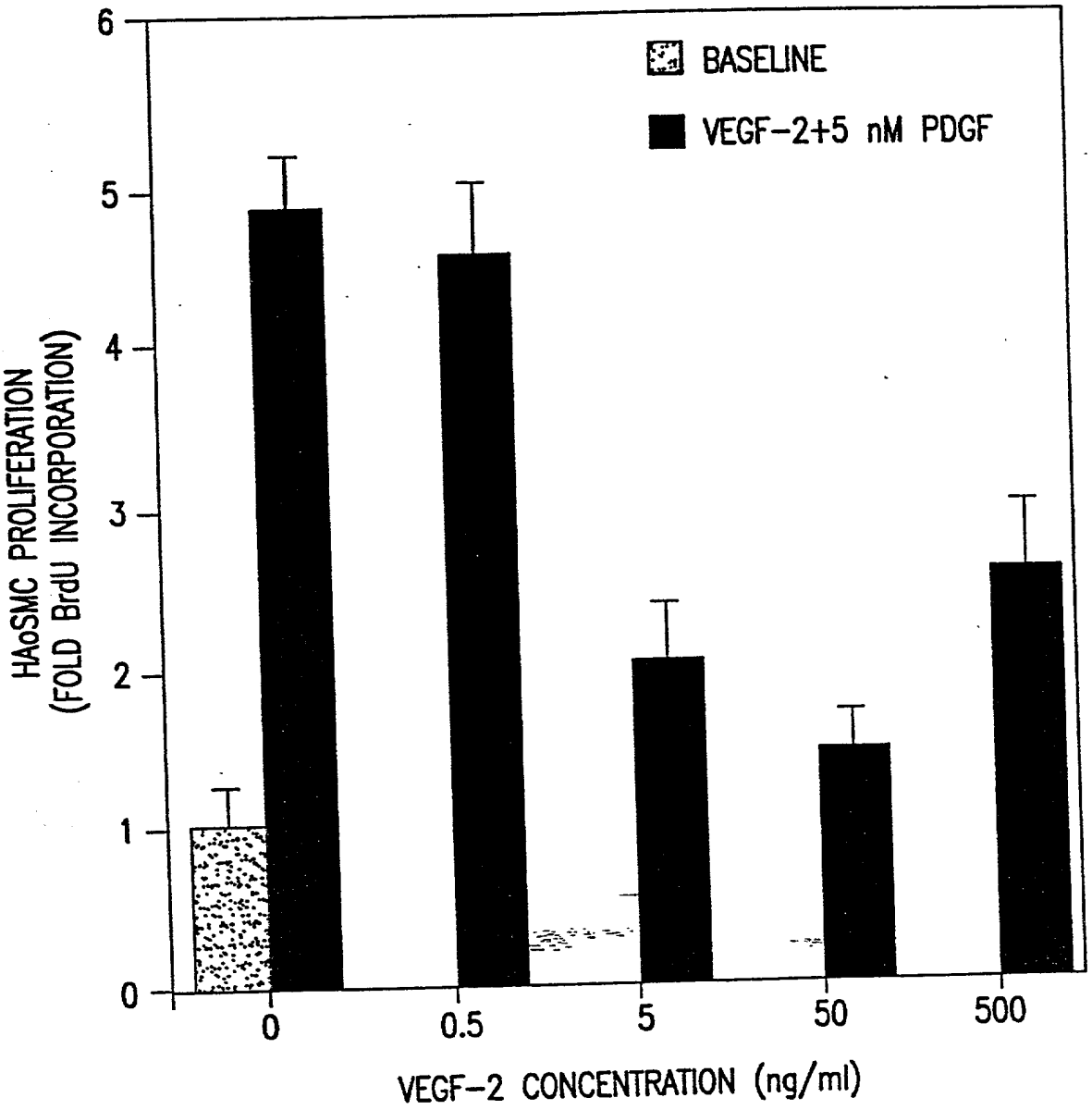

BASELINE
VEGF-2+5 nM PDGF
HAoSMC PROLIFERATION
(FOLD BrdU INCORPORATION)
0
1
2
3
4
5
6
0
0.5
5
50
500
VEGF-2 CONCENTRATION (ng/ml)

FIG.20A

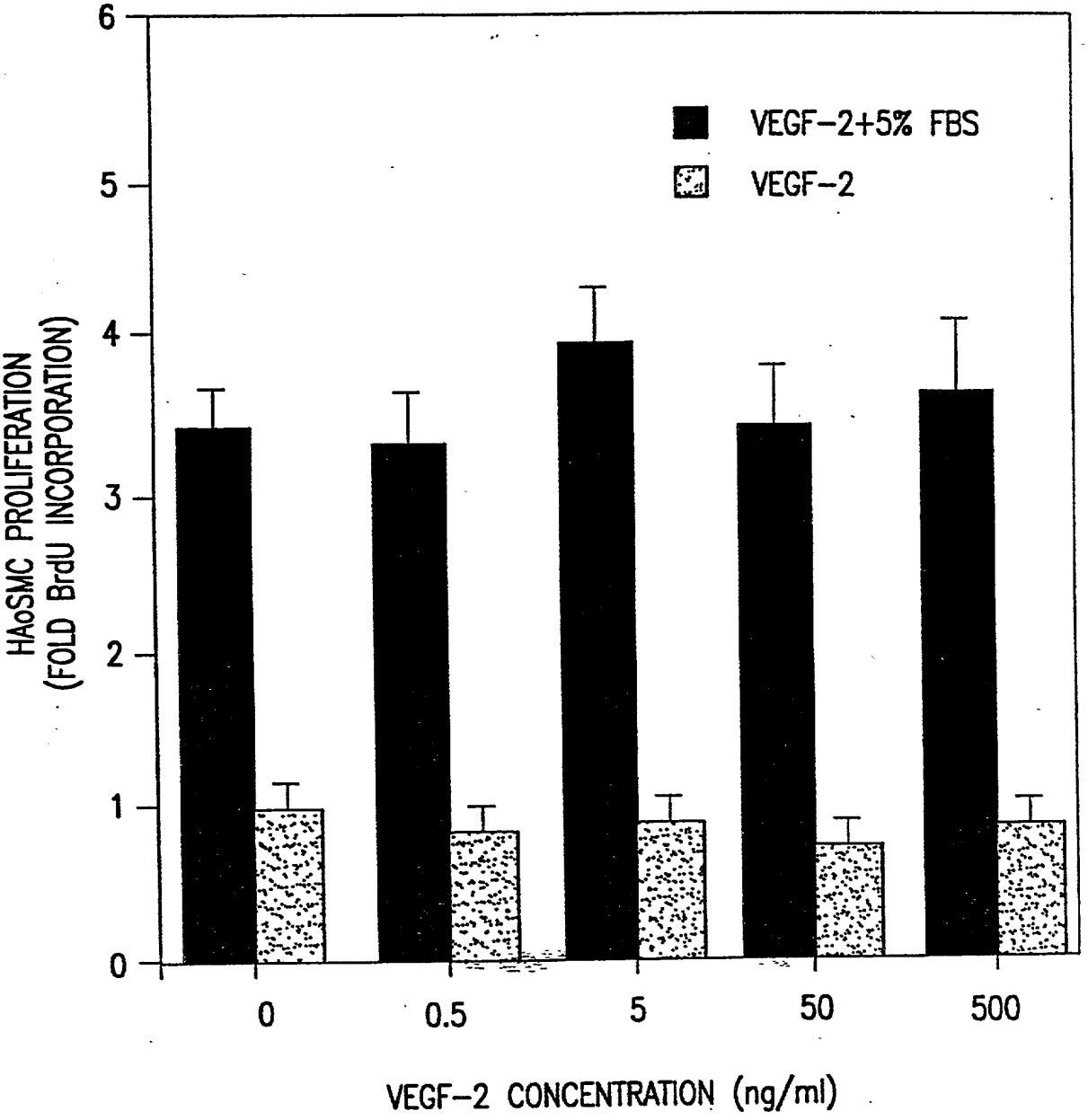

6
5
4
3
2
1
0
VEGF-2+5% FBS
VEGF-2
HAoSMC PROLIFERATION
(FOLD BrdU INCORPORATION)
0
0.5
5
50
500
VEGF-2 CONCENTRATION (ng/ml)

FIG.20B

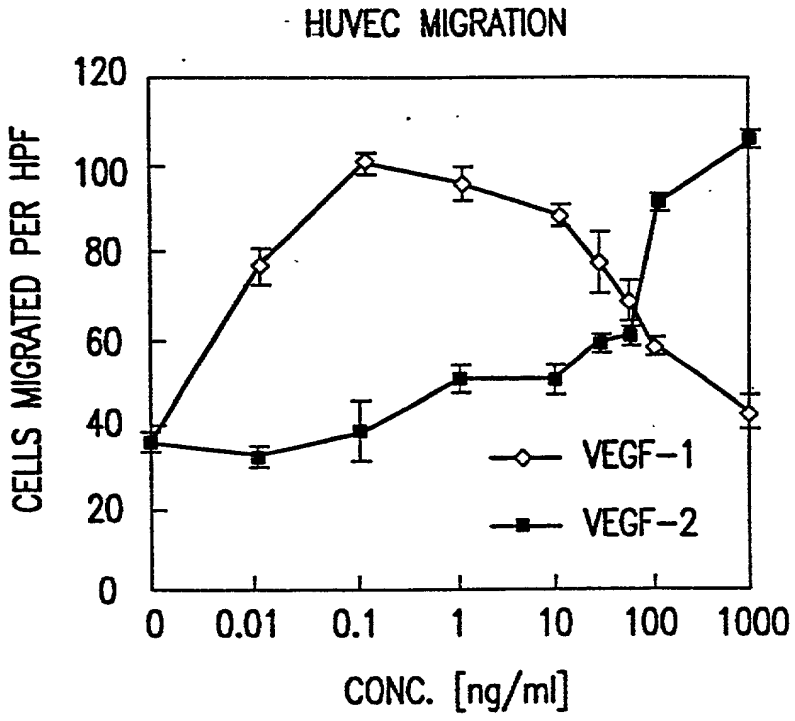


FIG.21A

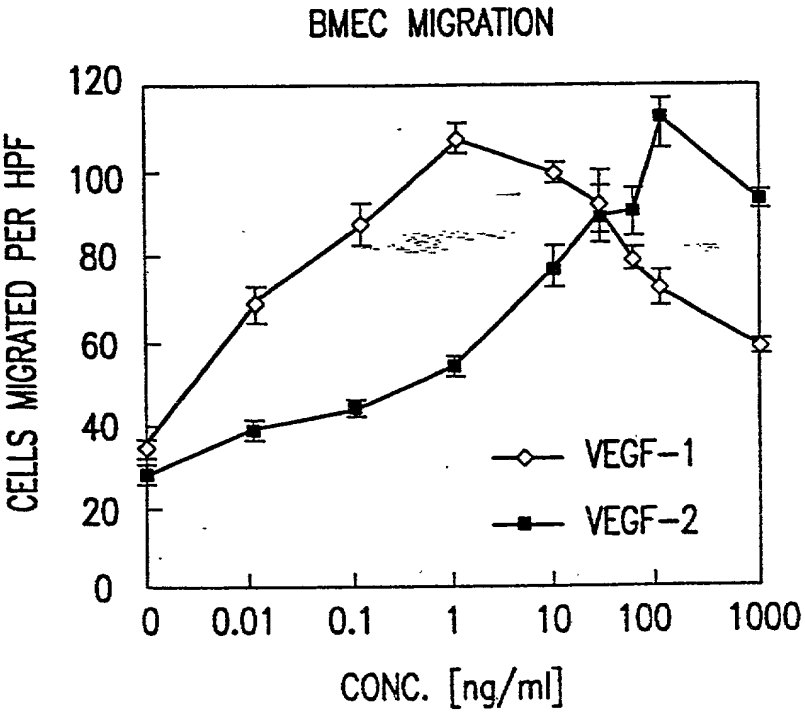


FIG.21B

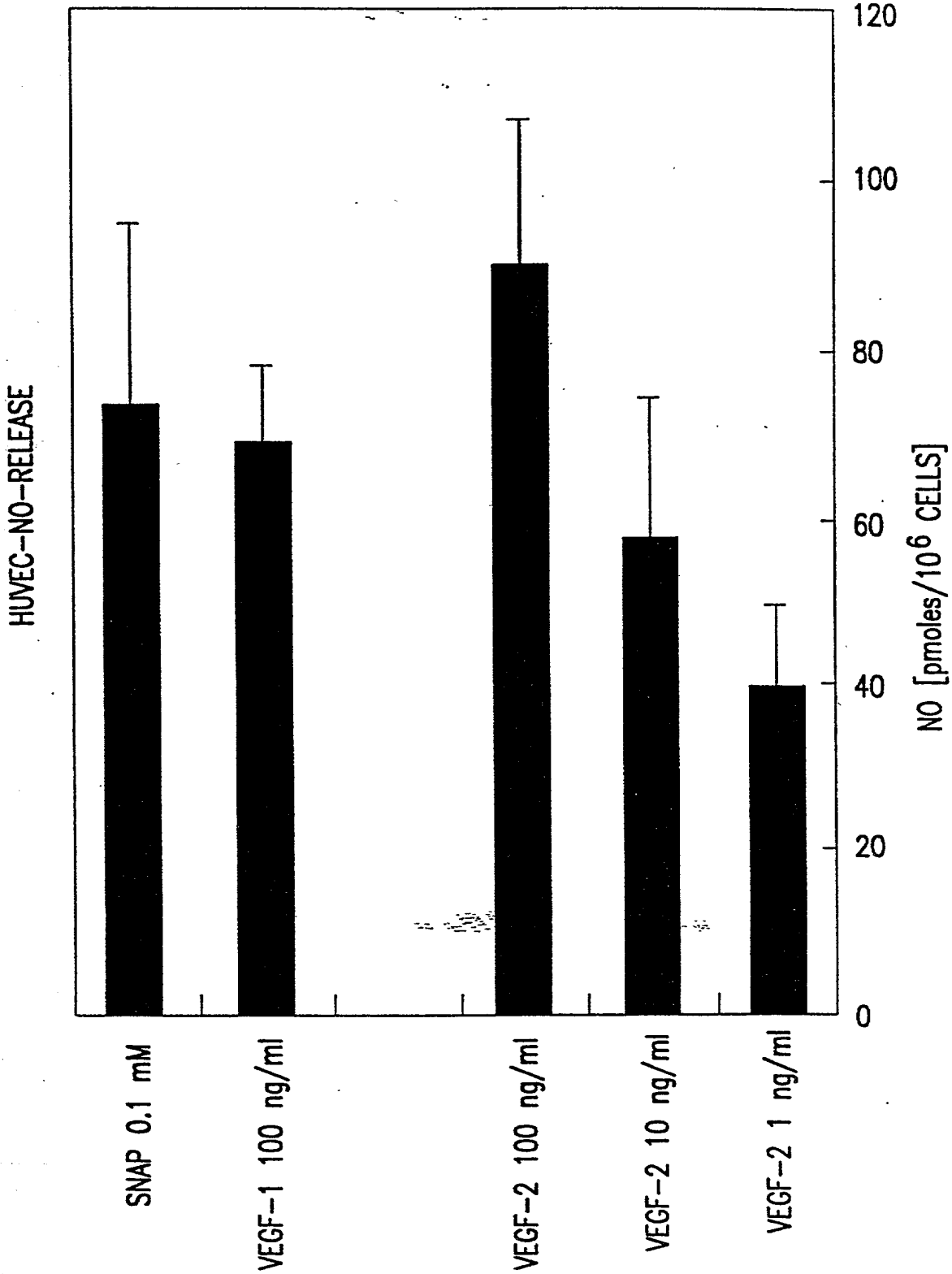

HUVEC-NO-RELEASE
NO [pmoles/10^6 CELLS]
120
100
80
60
40
20
0
SNAP 0.1 mM
VEGF-1 100 ng/ml
VEGF-2 100 ng/ml
VEGF-2 10 ng/ml
VEGF-2 1 ng/ml

FIG.22

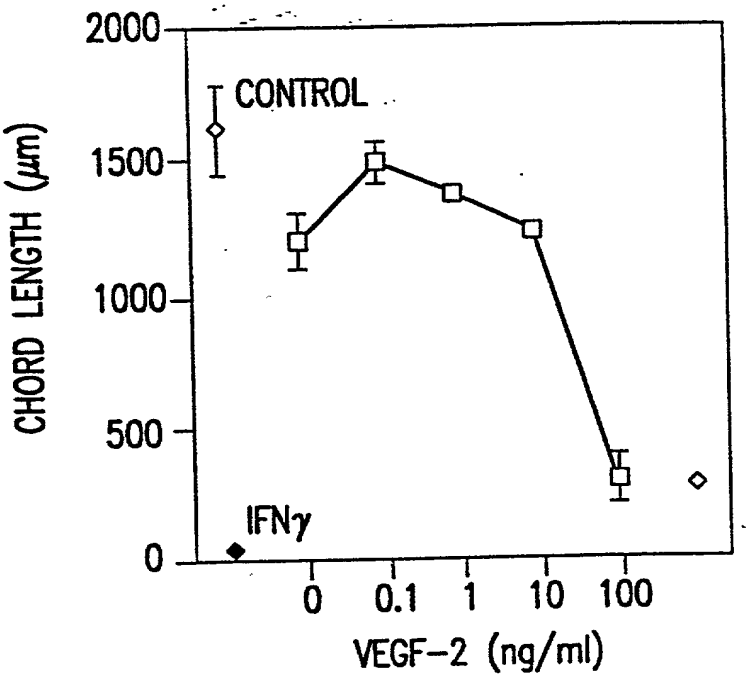

2000
1500
1000
500
0
CHORD LENGTH (μm)
CONTROL
IFNγ
0
0.1
1
10
100
VEGF-2 (ng/ml)

FIG.23

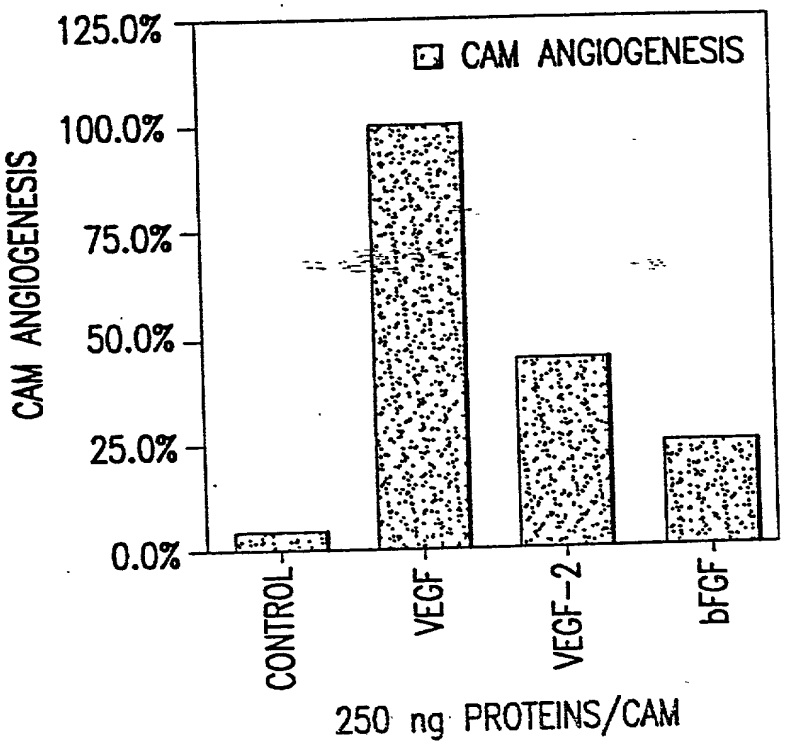

125.0%
100.0%
75.0%
50.0%
25.0%
0.0%
CAM ANGIOGENESIS
CAM ANGIOGENESIS
CONTROL
VEGF
VEGF-2
bFGF
250 ng PROTEINS/CAM

FIG.24

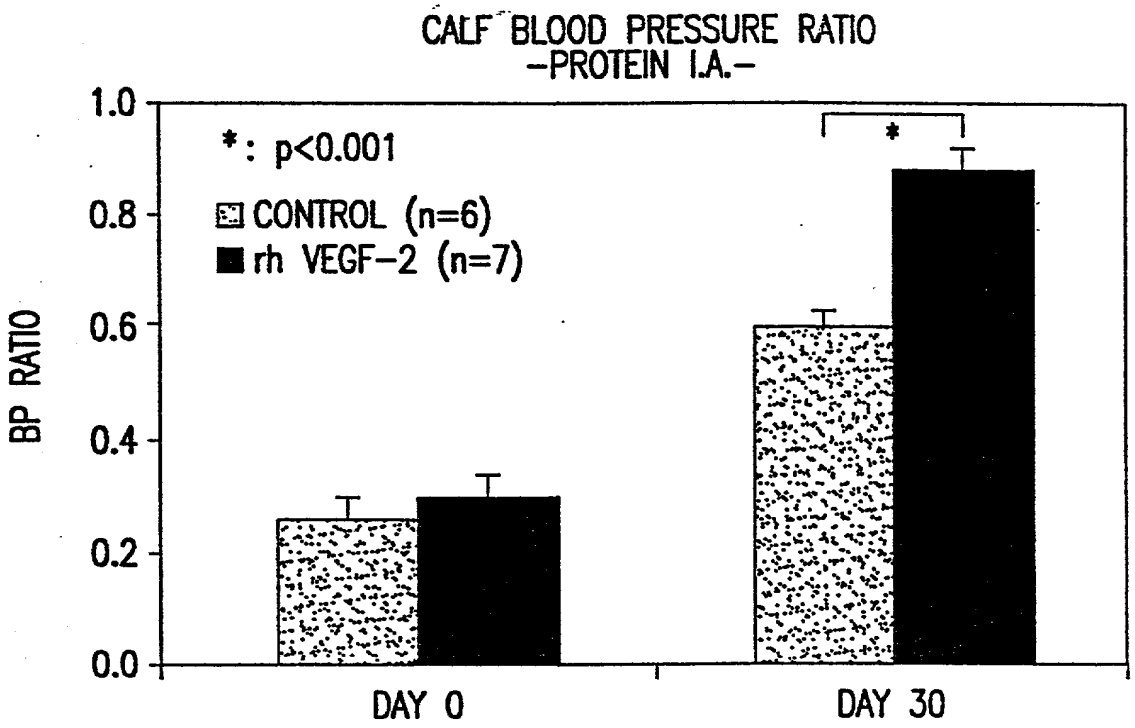


FIG.25A

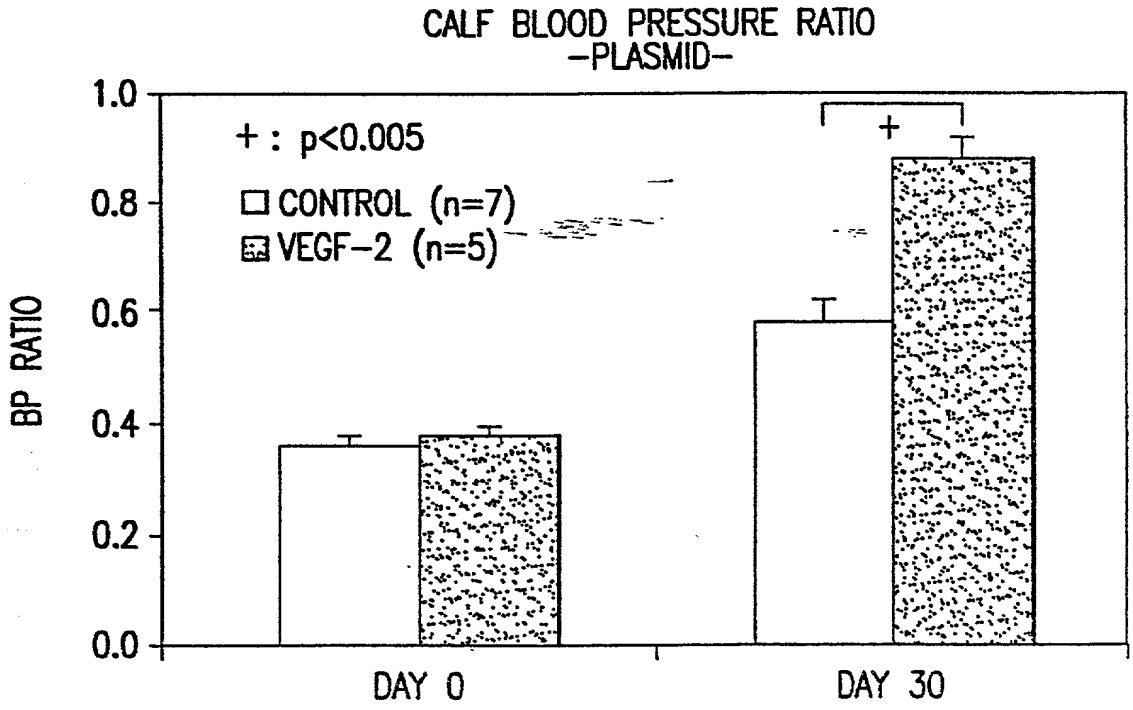


FIG.25B

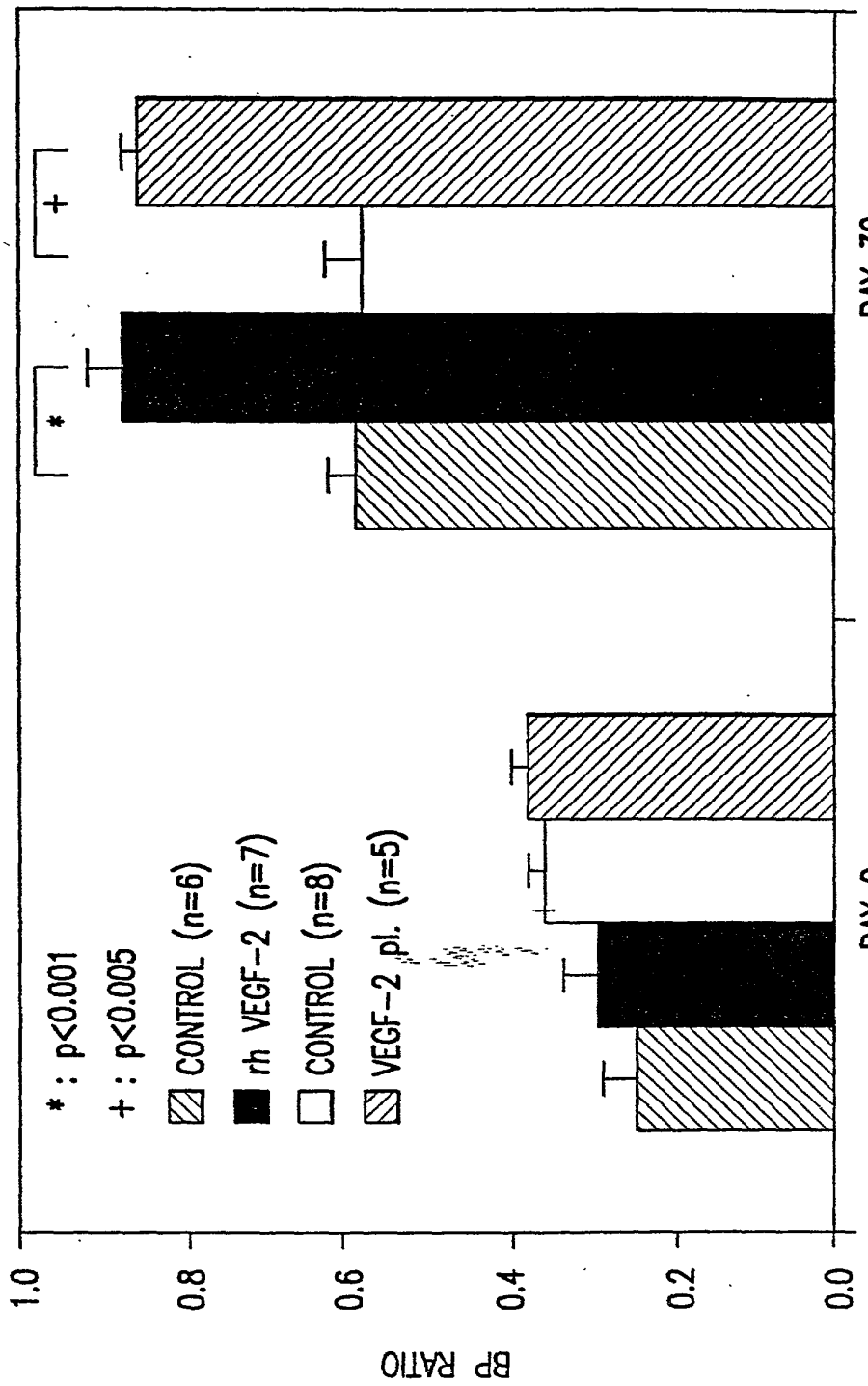

CALF BLOOD PRESSURE RATIO
*: p<0.001
+: p<0.005
CONTROL (n=6)
rh VEGF-2 (n=7)
CONTROL (n=8)
VEGF-2 pl. (n=5)
BP RATIO
1.0
0.8
0.6
0.4
0.2
0.0
DAY 0
DAY 30

FIG.25C

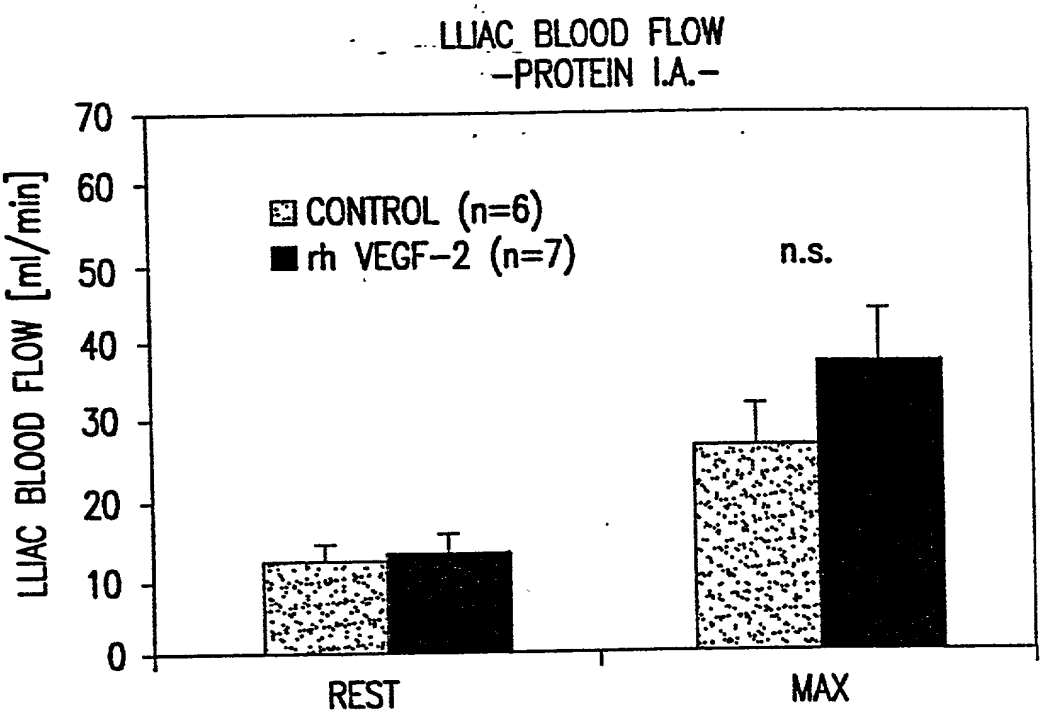


FIG.25D

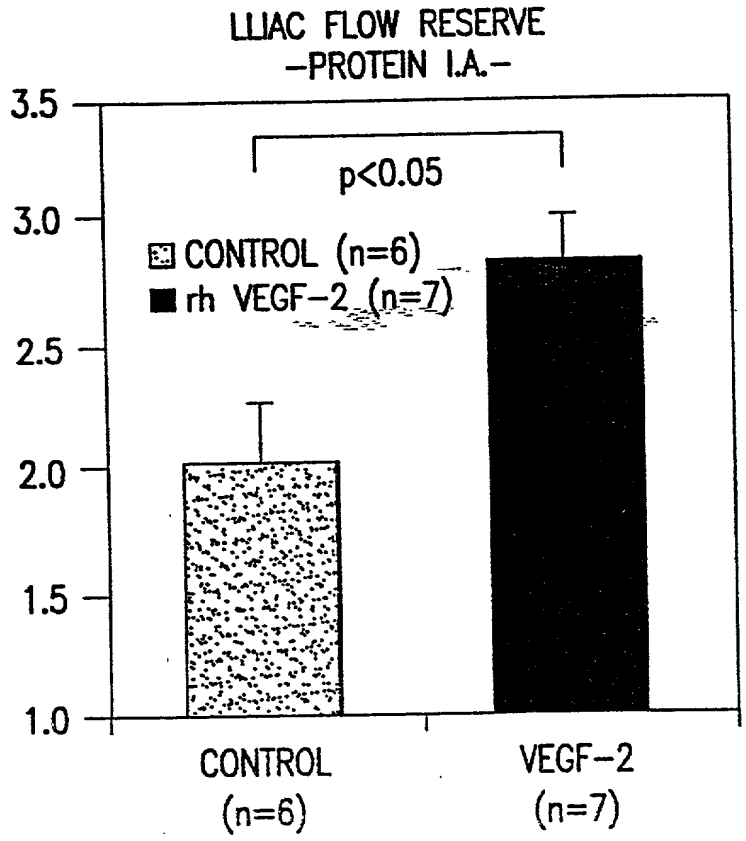


FIG.25E

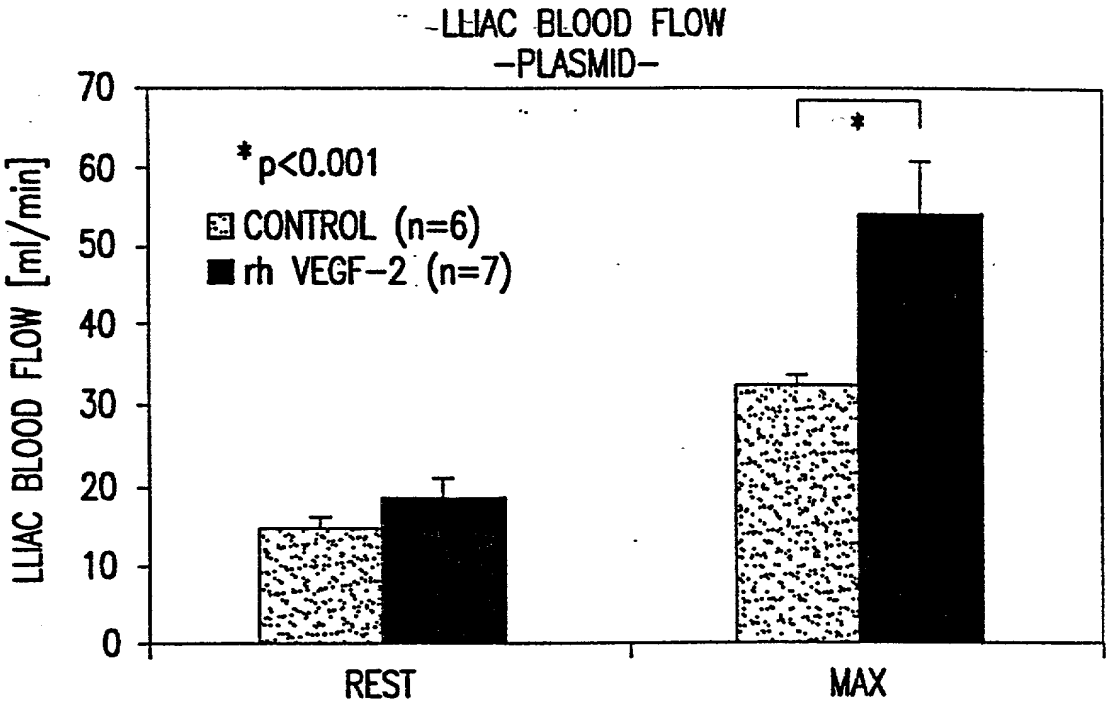


FIG.25F

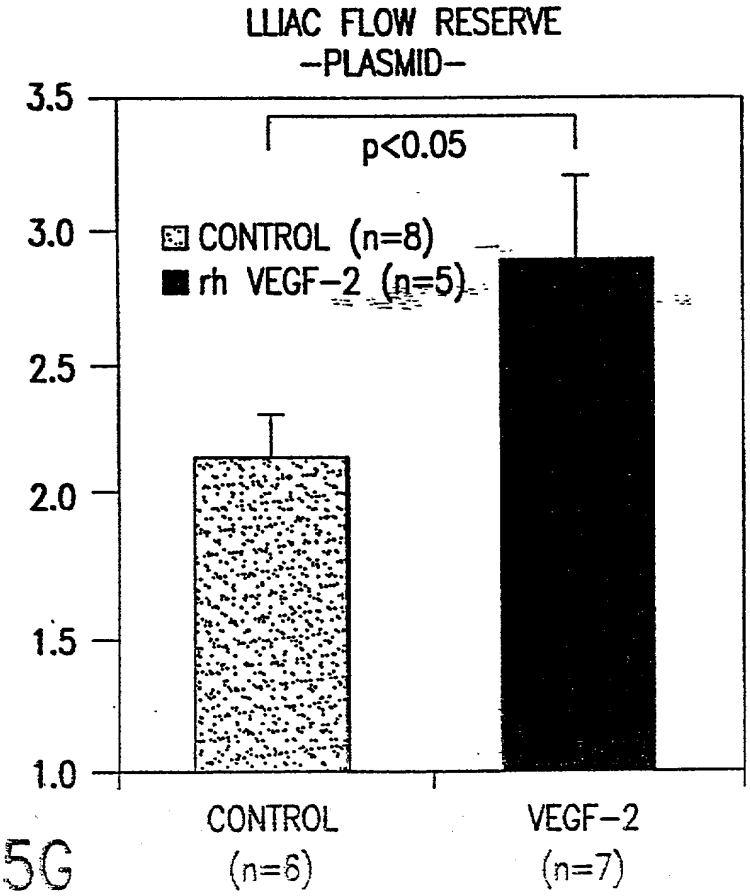


FIG.25G

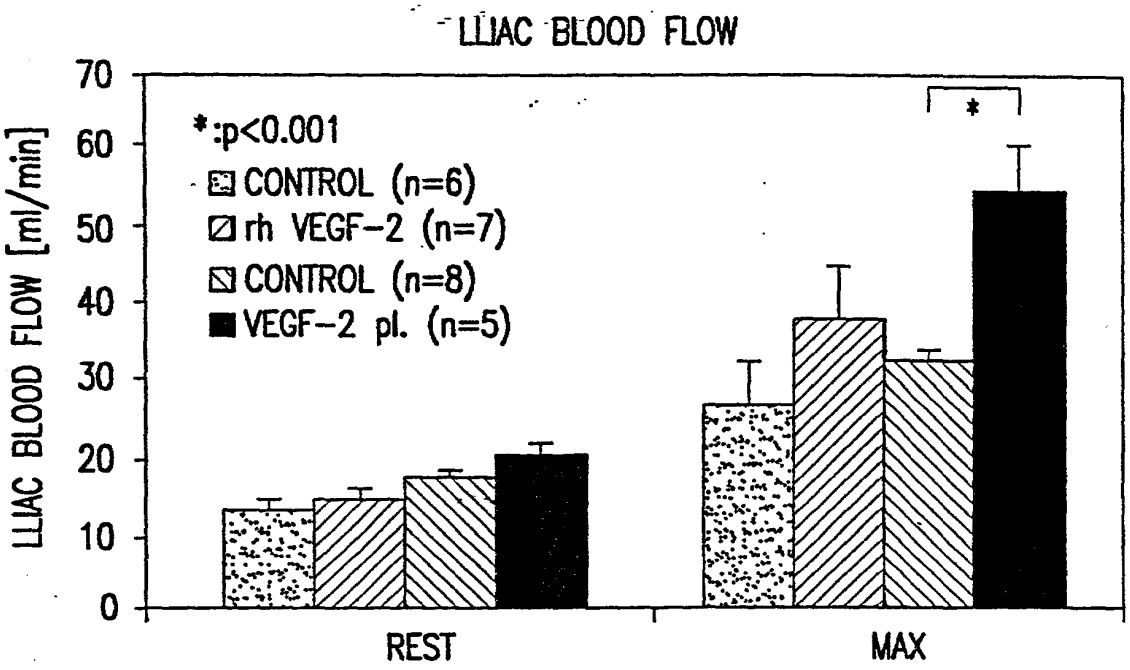


FIG.25H

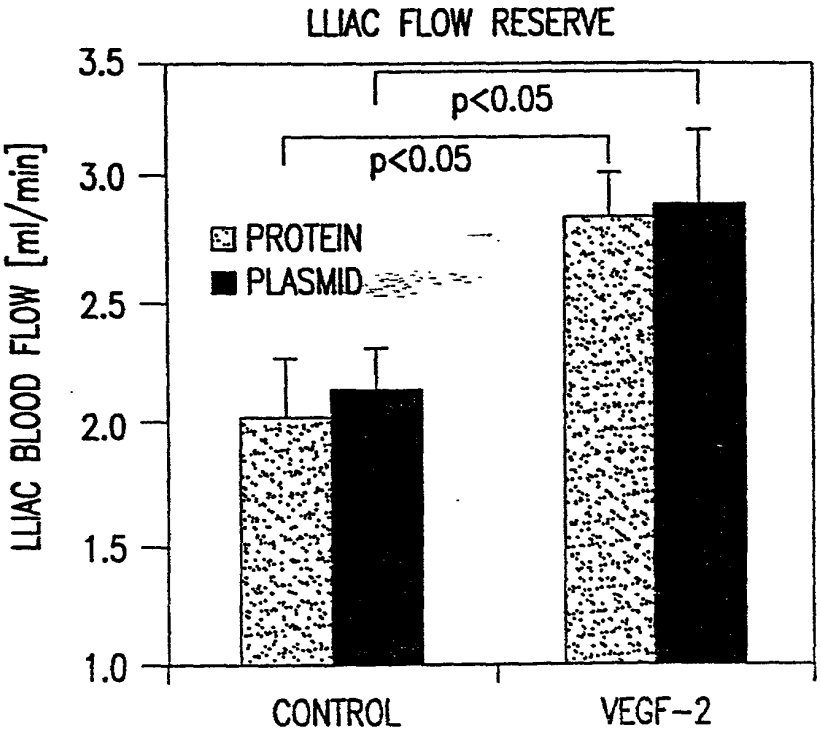


FIG.25I

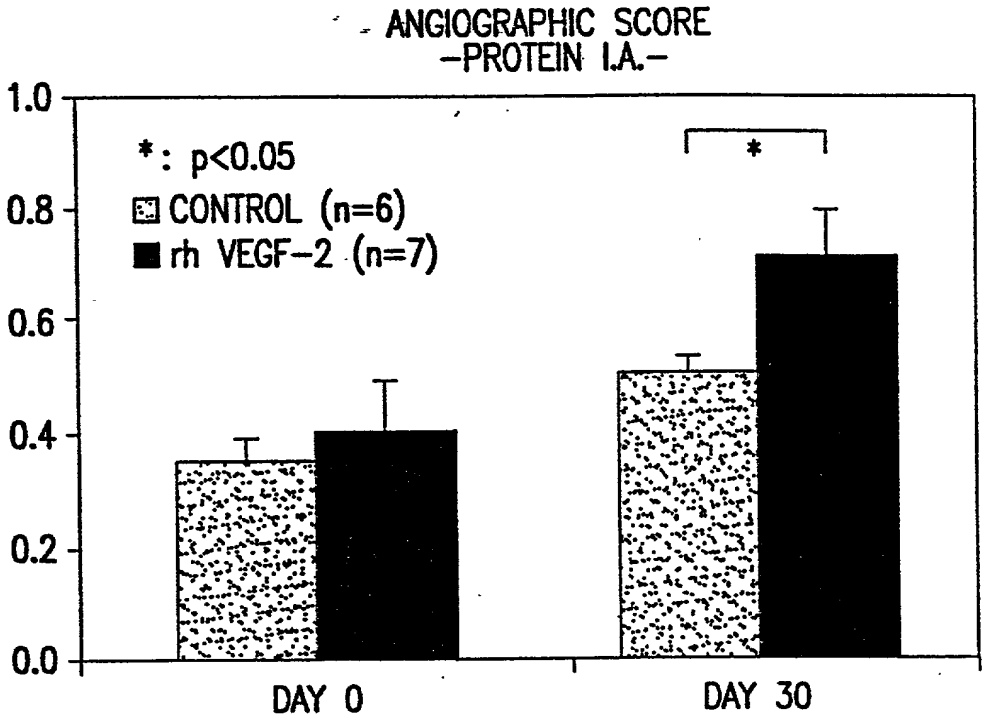


FIG.25J

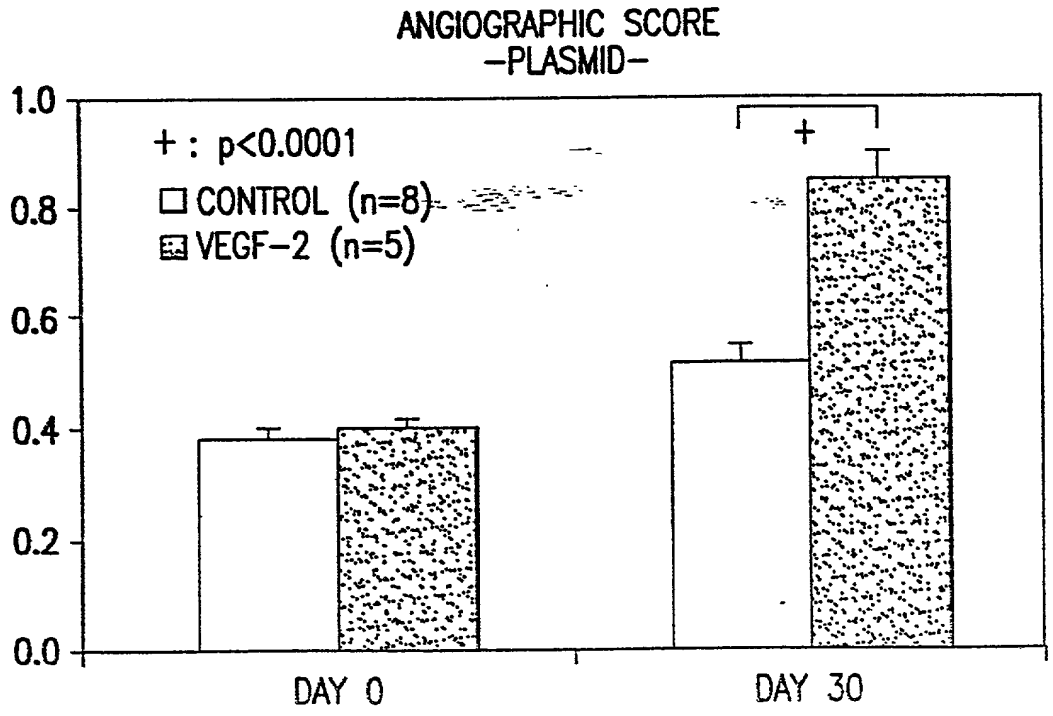


FIG.25K

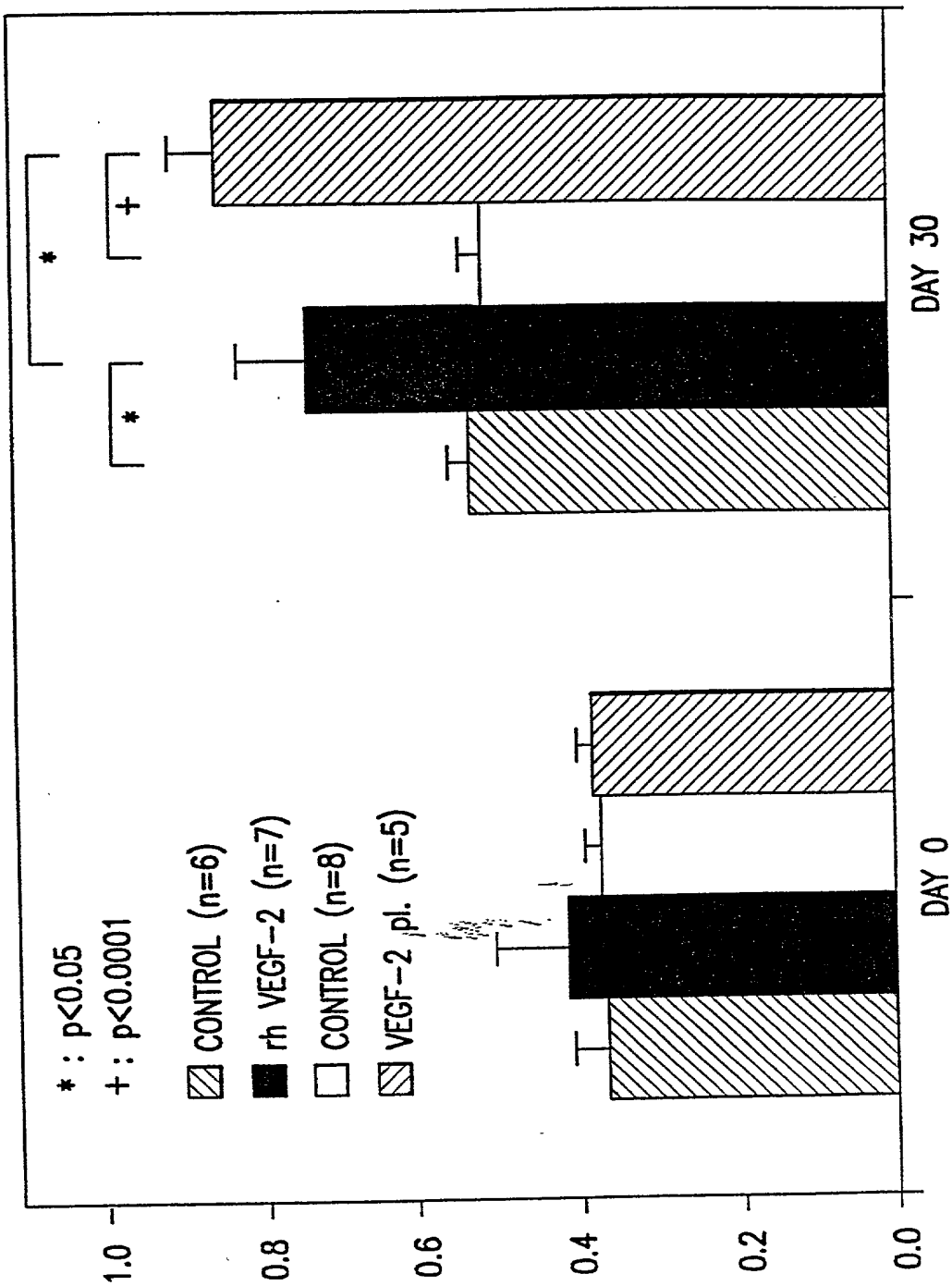

ANGIOGRAPHIC SCORE
1.0
0.8
0.6
0.4
0.2
0.0
*
+
*
+
DAY 0
DAY 30
*: p<0.05
+: p<0.0001
CONTROL (n=6)
rh VEGF-2 (n=7)
CONTROL (n=8)
VEGF-2 pl. (n=5)

FIG.25L

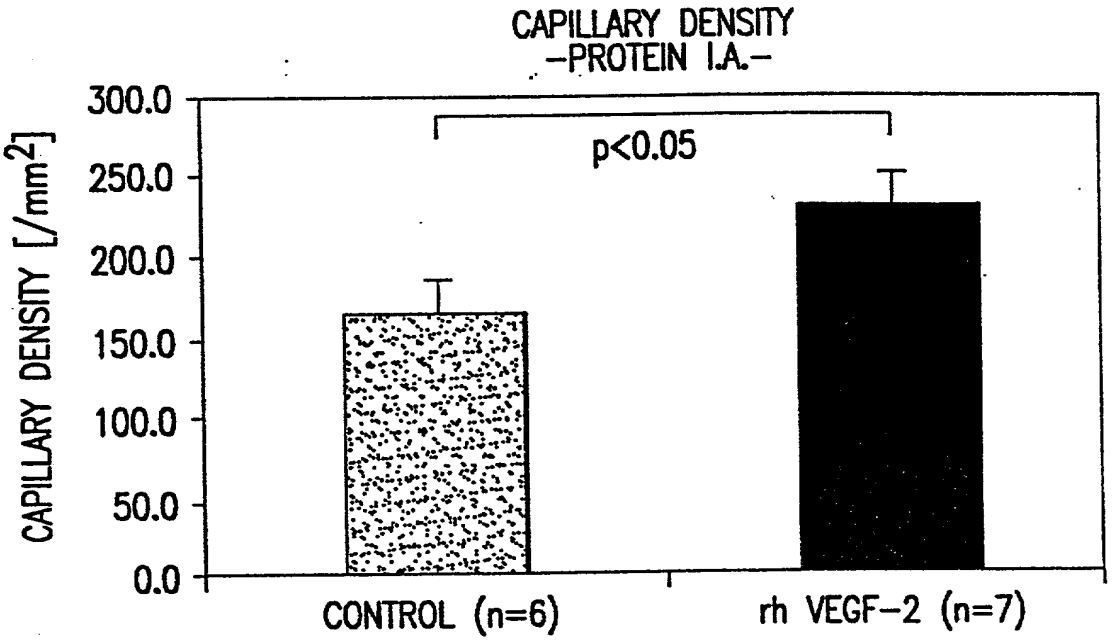


FIG.25M

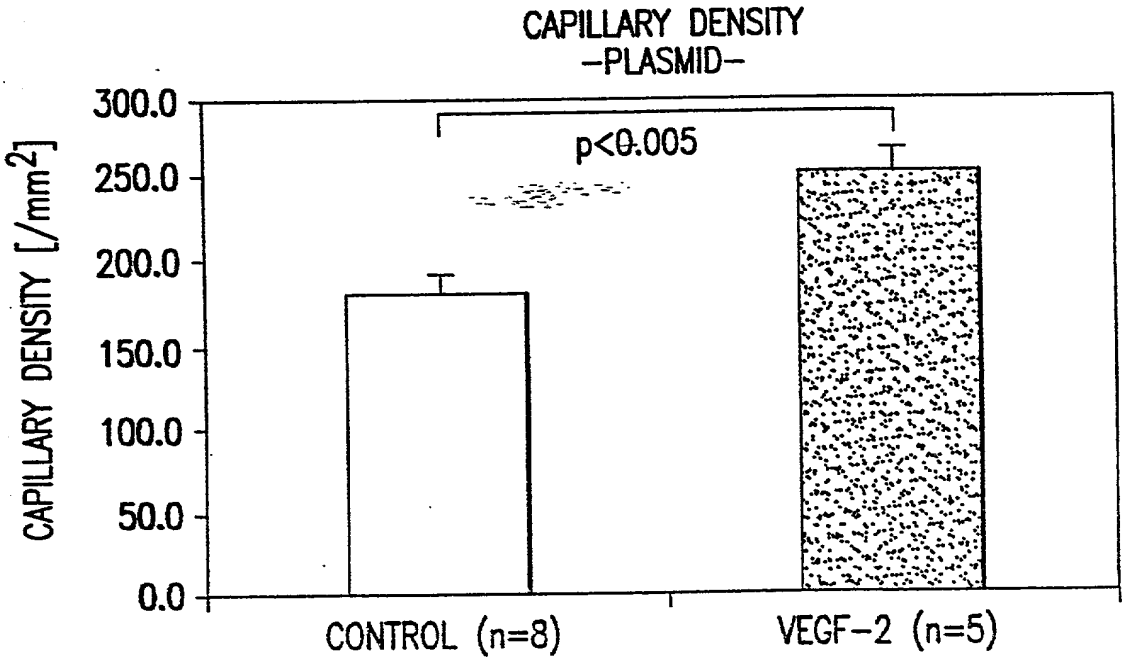


FIG.25N

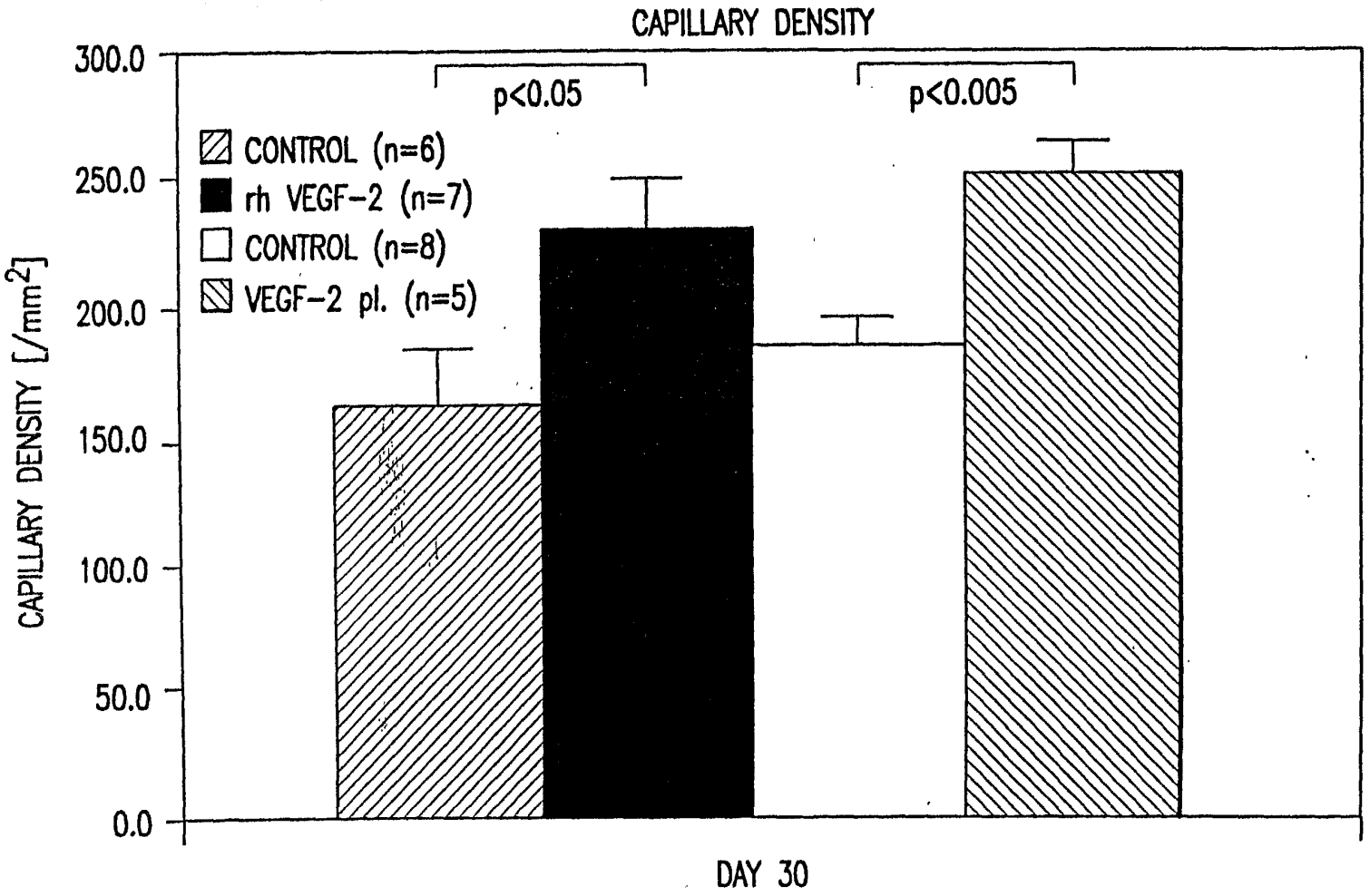


FIG.25 O

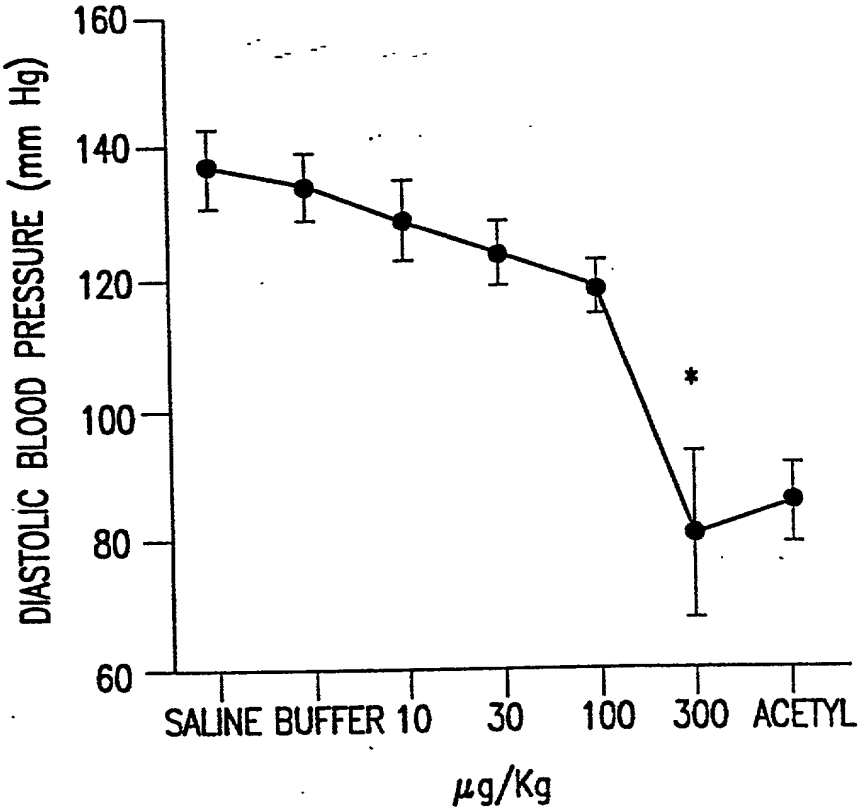


FIG.26A

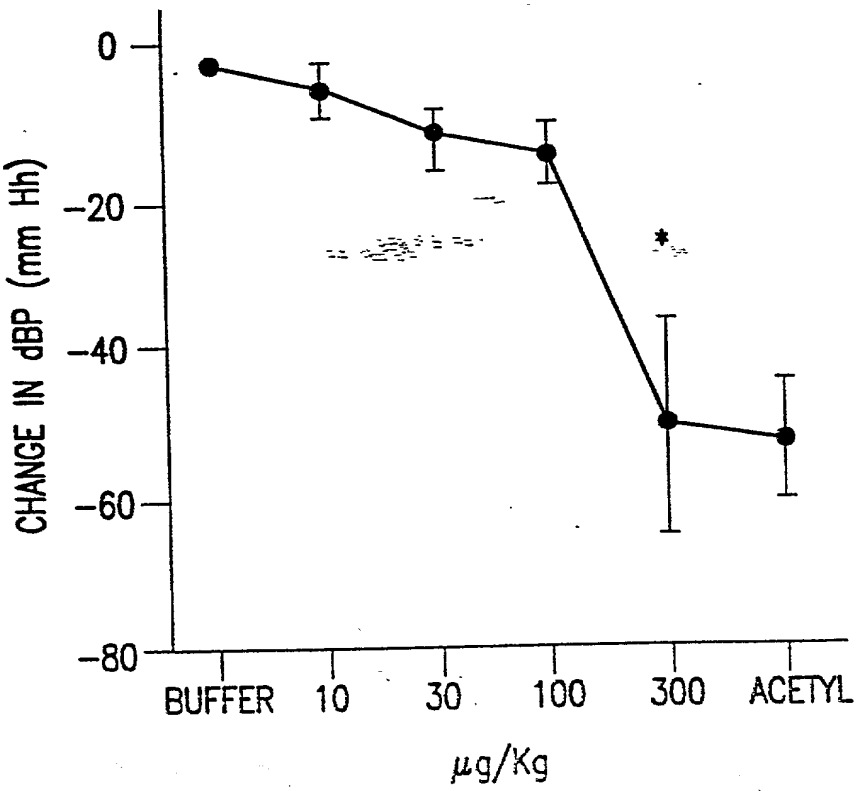


FIG.26B

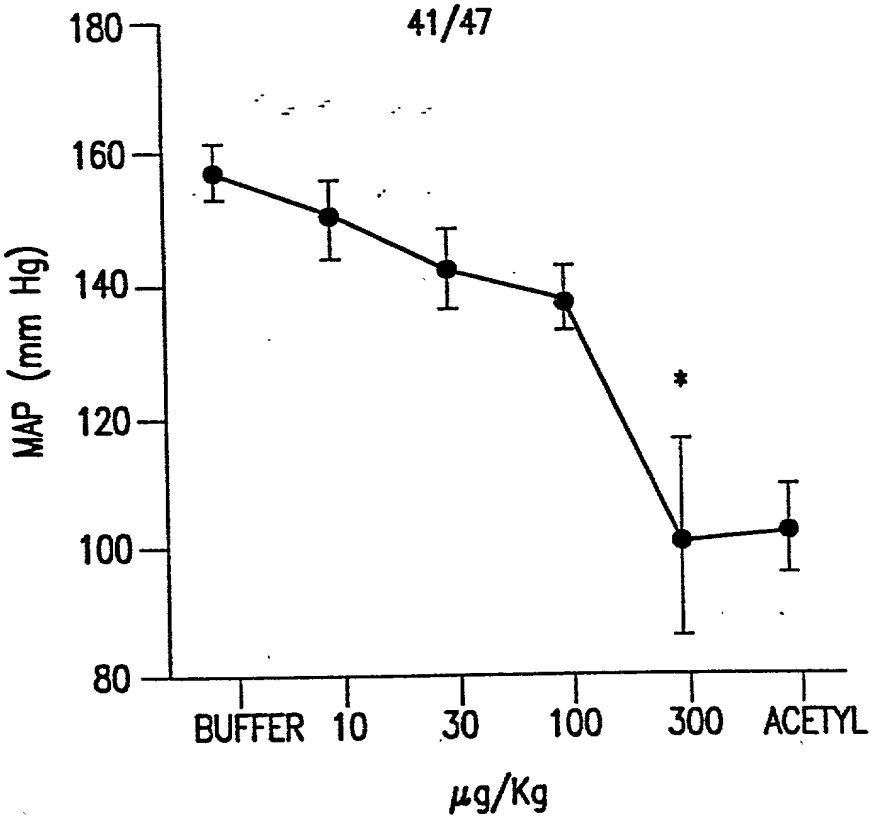


FIG.26C

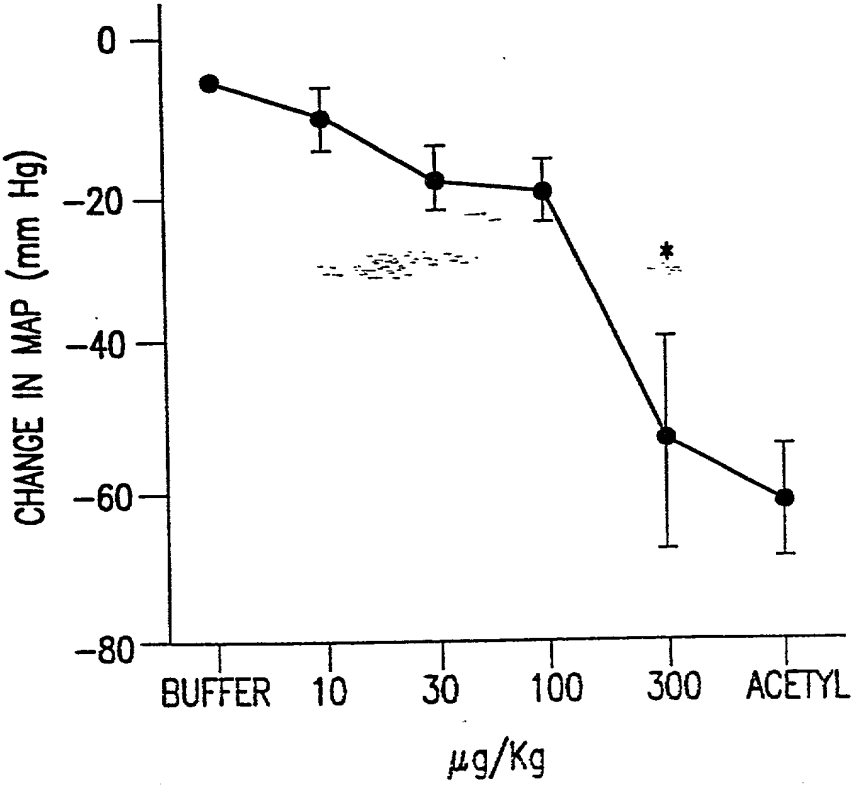


FIG.26D

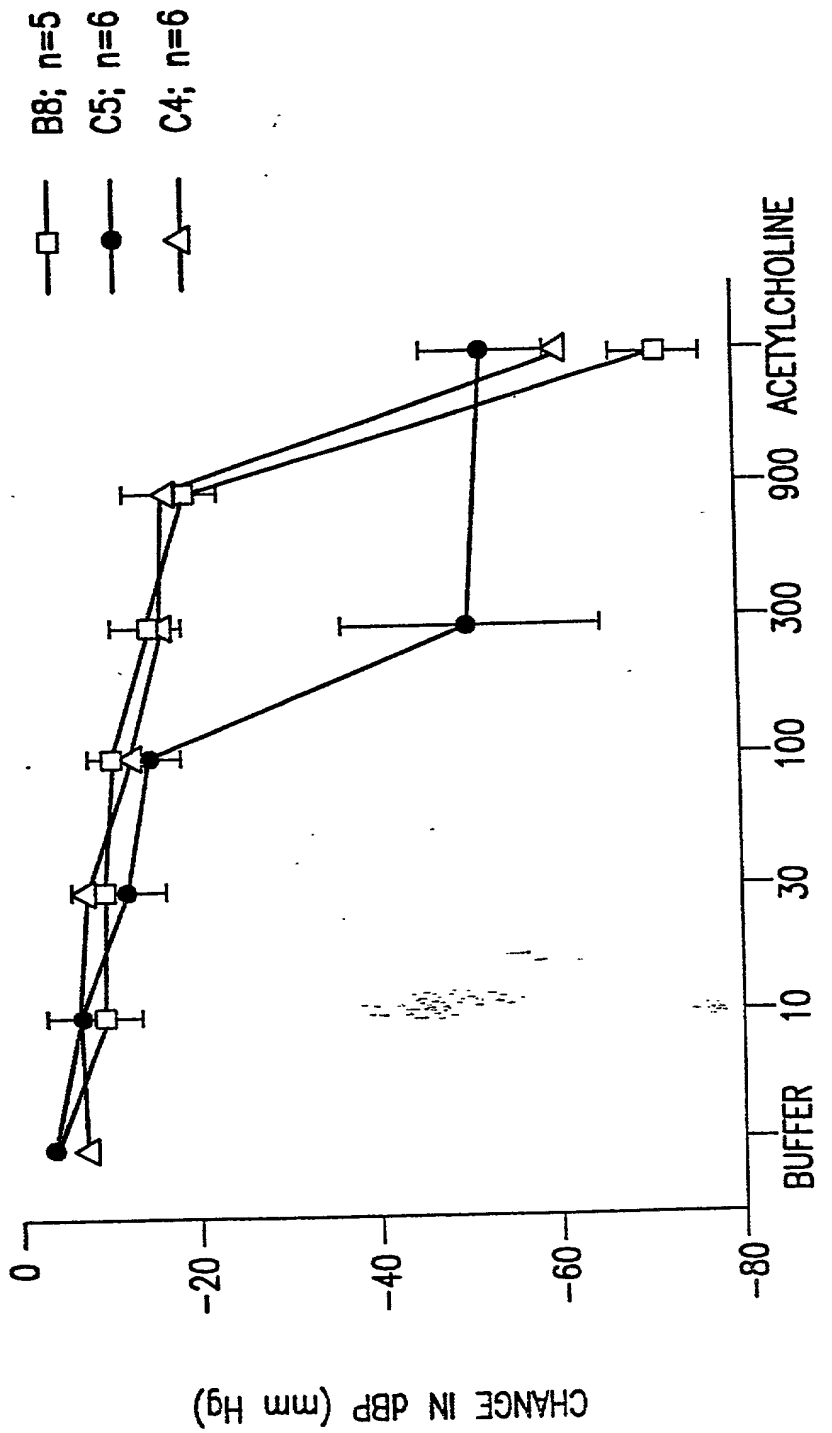

CHANGE IN DIASTOLIC BLOOD PRESSURE OF SHR RATS GIVEN INCREASING DOSES OF VEGF-2
B8; n=5
C5; n=6
C4; n=6
CHANGE IN dBP (mm Hg)
0
-20
-40
-60
-80
BUFFER
10
30
100
300
900
ACETYLCHOLINE
μg/Kg

FIG.26E

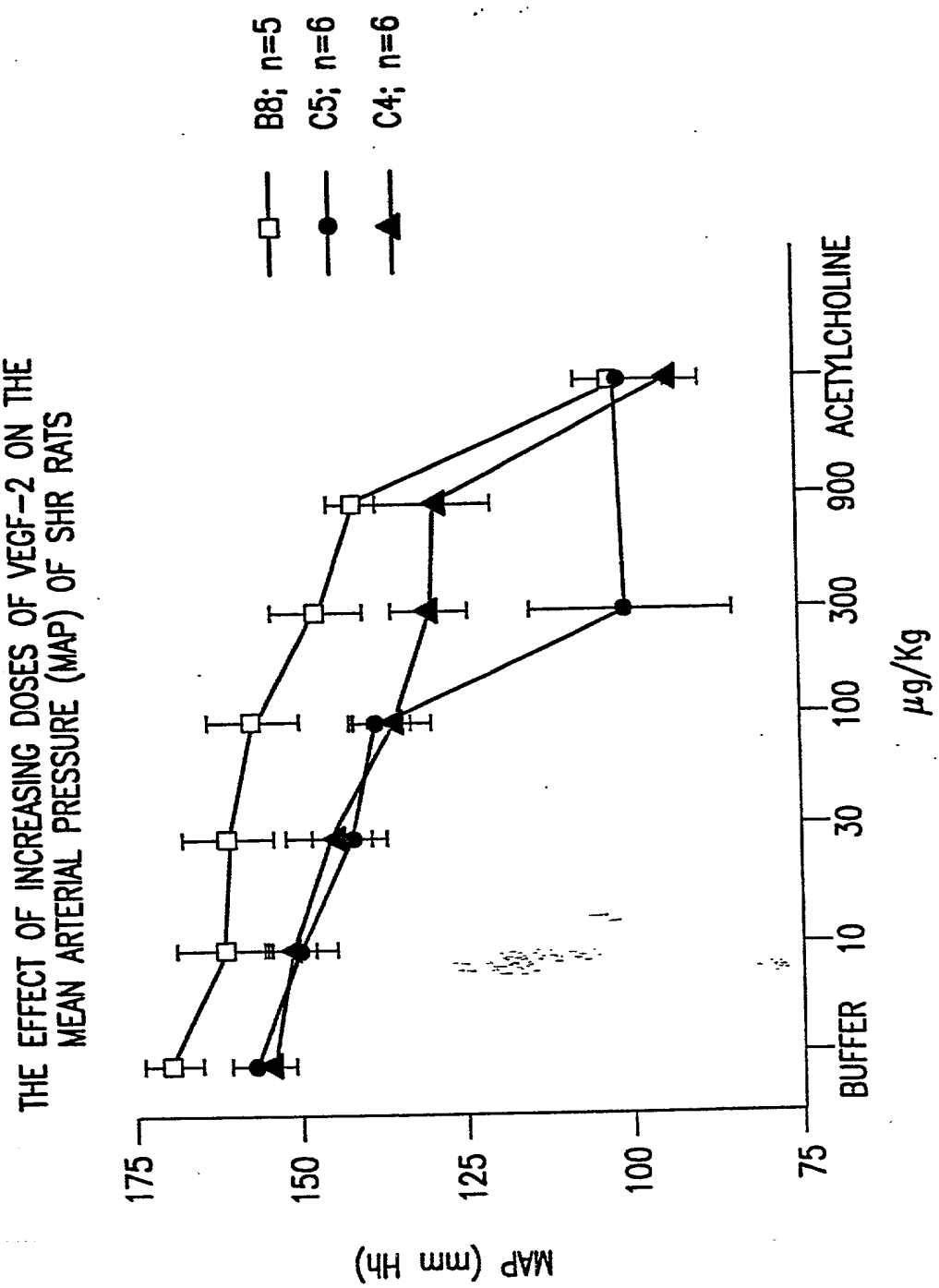

THE EFFECT OF INCREASING DOSES OF VEGF-2 ON THE MEAN ARTERIAL PRESSURE (MAP) OF SHR RATS
B8; n=5
C5; n=6
C4; n=6
MAP (mm Hh)
175
150
125
100
75
BUFFER
10
30
100
300
900
ACETYLCHOLINE
µg/Kg

FIG.26F

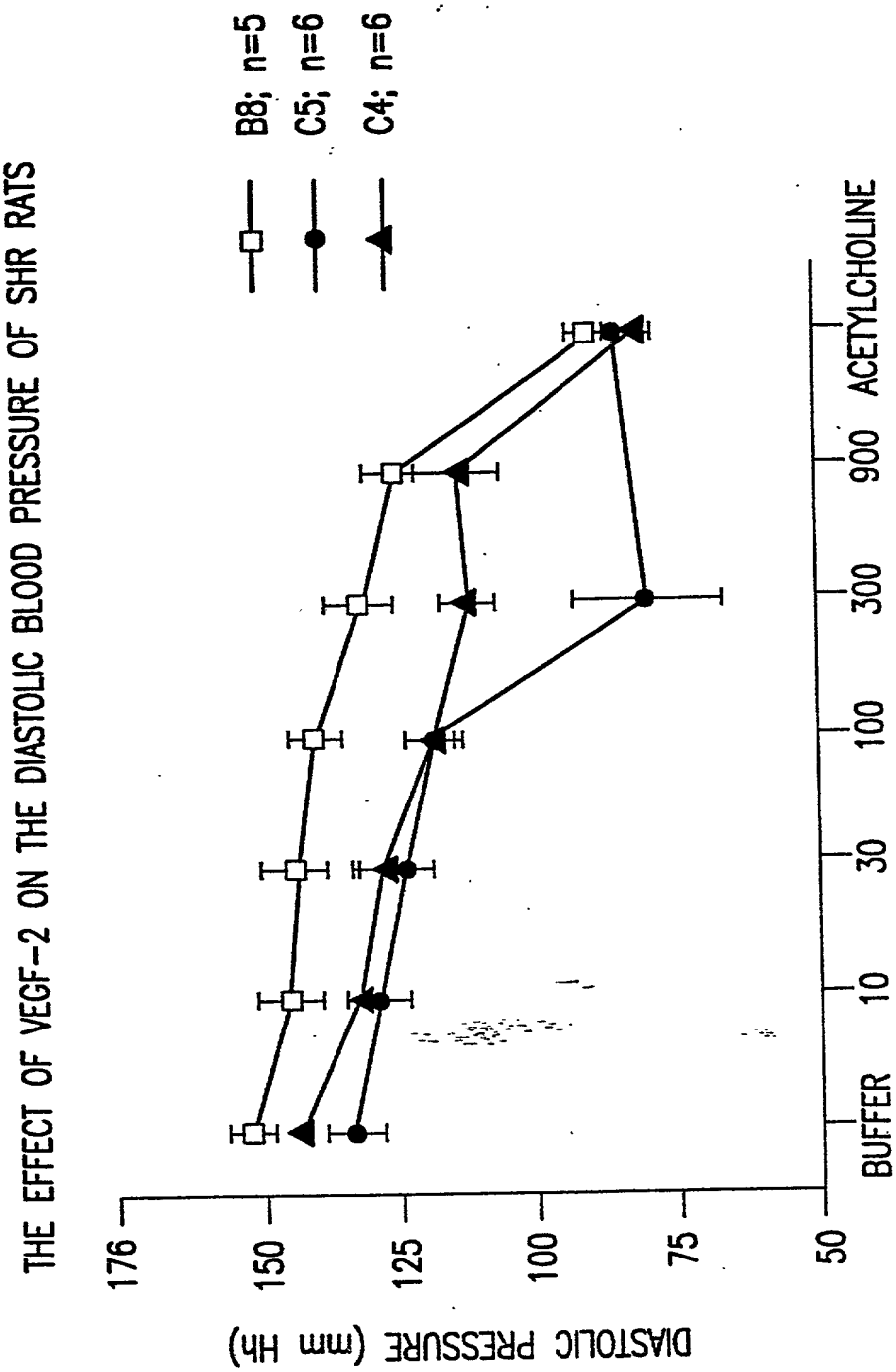

THE EFFECT OF VEGF-2 ON THE DIASTOLIC BLOOD PRESSURE OF SHR RATS
B8; n=5
C5; n=6
C4; n=6
DIASTOLIC PRESSURE (mm Hg)
176
150
125
100
75
50
BUFFER
10
30
100
300
900
ACETYLCHOLINE

FIG.26G

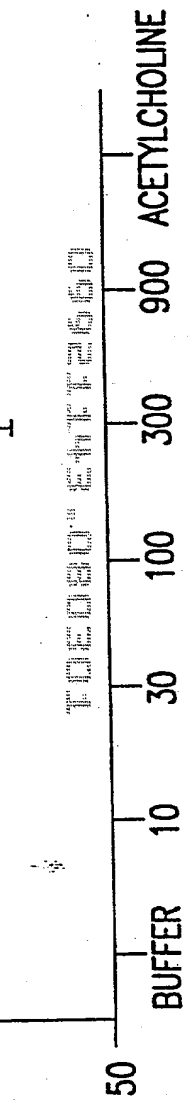


FIG.26G

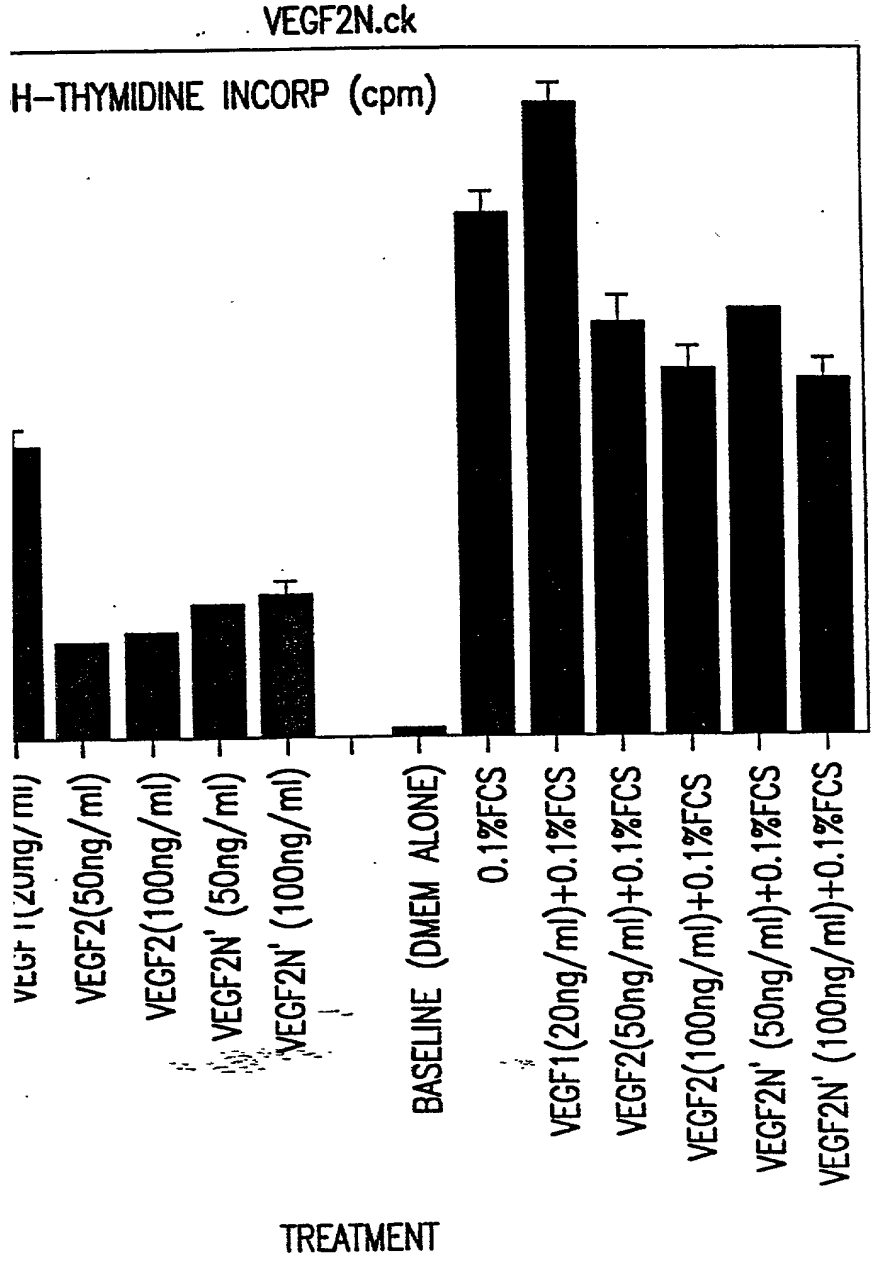


FIG.27

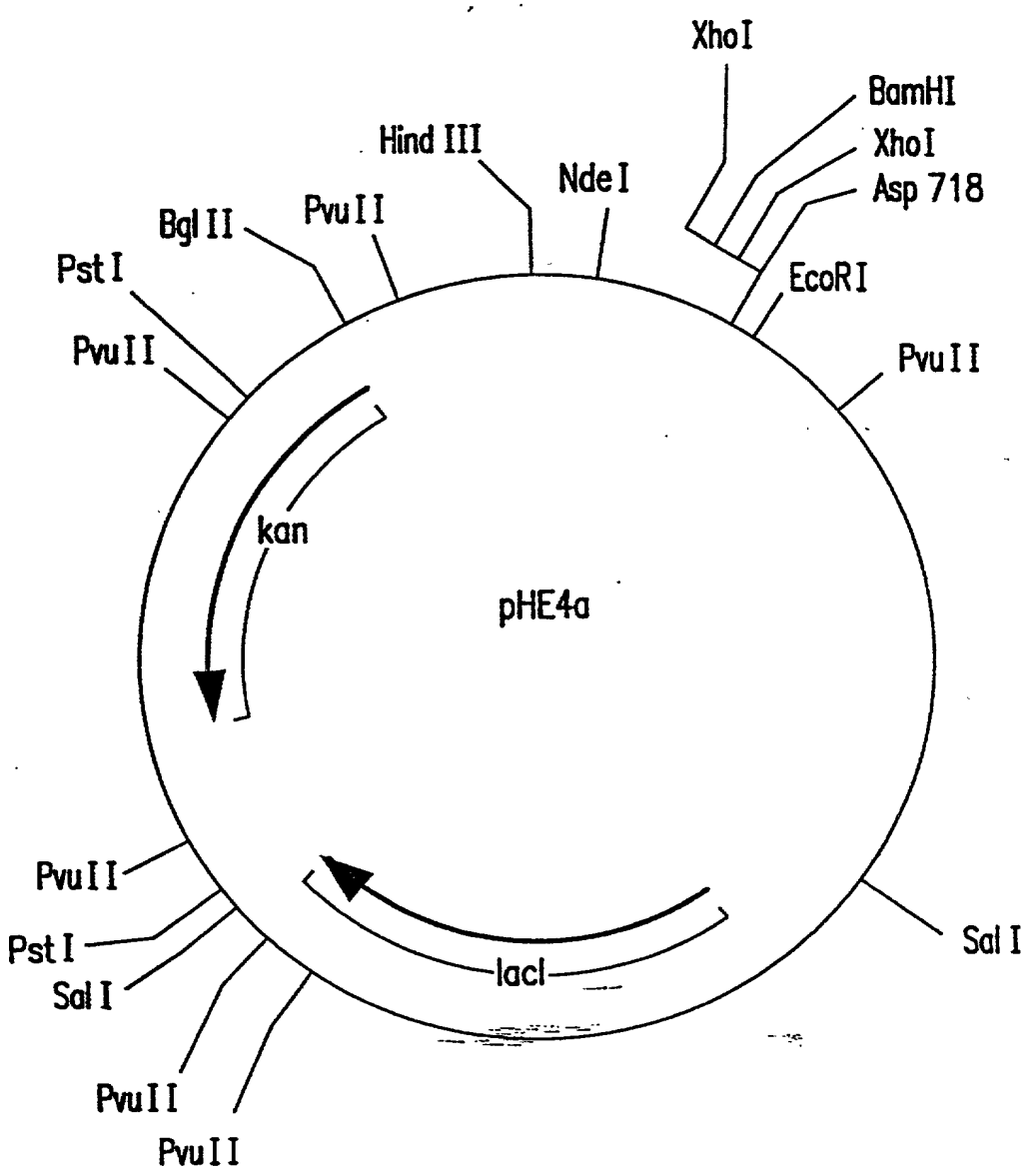

XhoI
BamHI
XhoI
Asp 718
Hind III
NdeI
BglII
PvuII
PstI
EcoRI
PvuII
PvuII
kan
pHE4a
PvuII
PstI
SalI
lacI
SalI
PvuII
PvuII

FIG.28

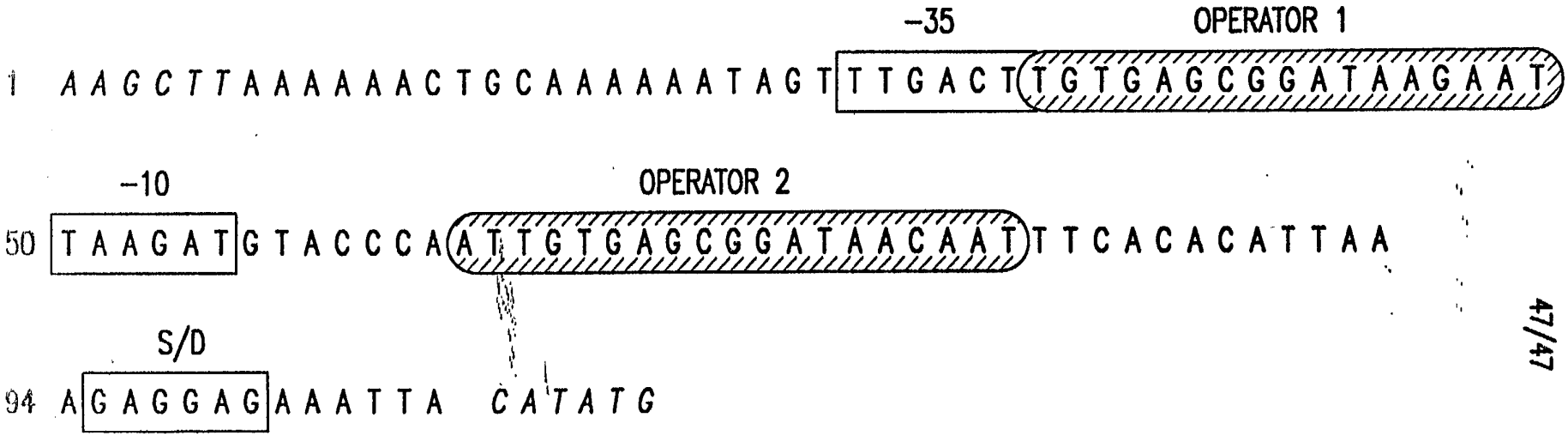


FIG.29

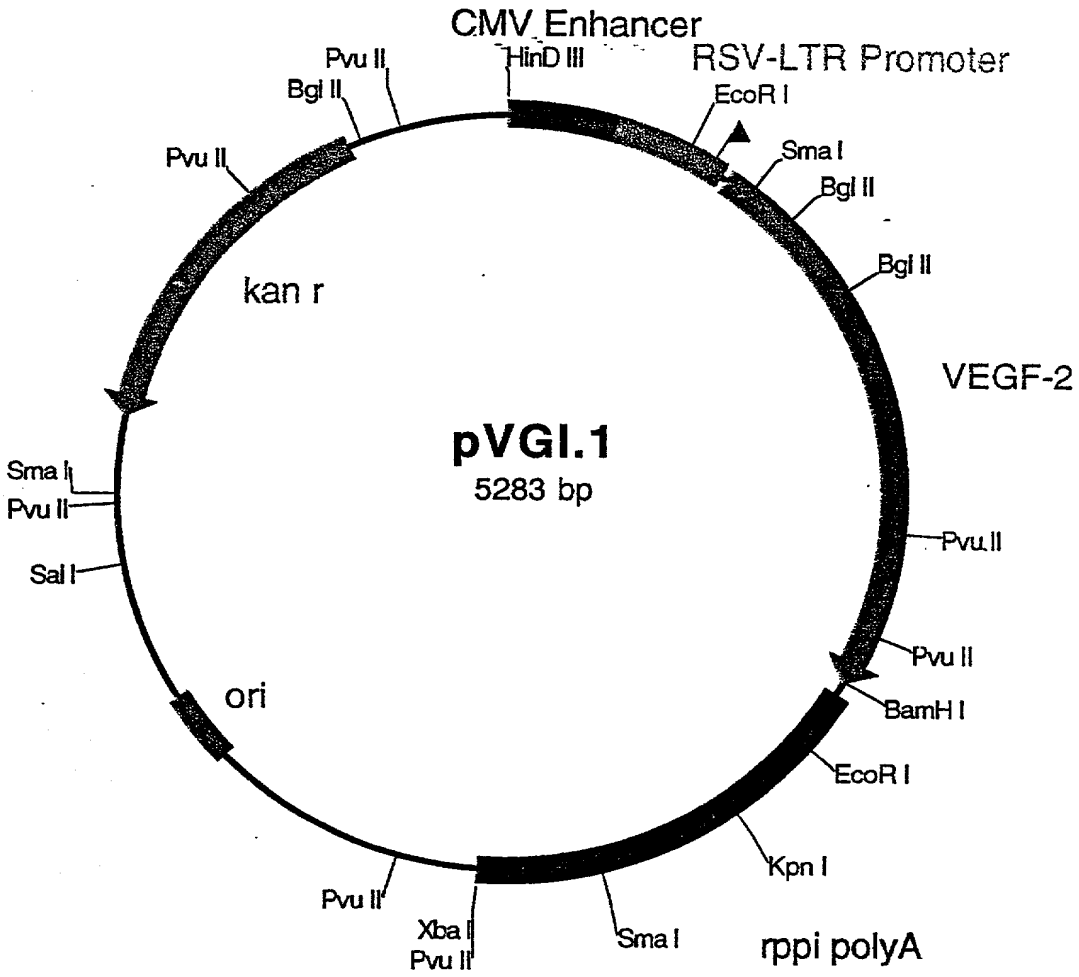

CMV Enhancer
RSV-LTR Promoter
HinD III
EcoR I
Sma I
Bgl II
Bgl II
VEGF-2
Pvu II
BamH I
EcoR I
Kpn I
Sma I
rppi polyA
Pvu II
Xba I
Pvu II
ori
Sal I
Sma I
Pvu II
Pvu II
Bgl II
Pvu II
kan r
pVGI.1
5283 bp

FIG. 30

FIG. 31A

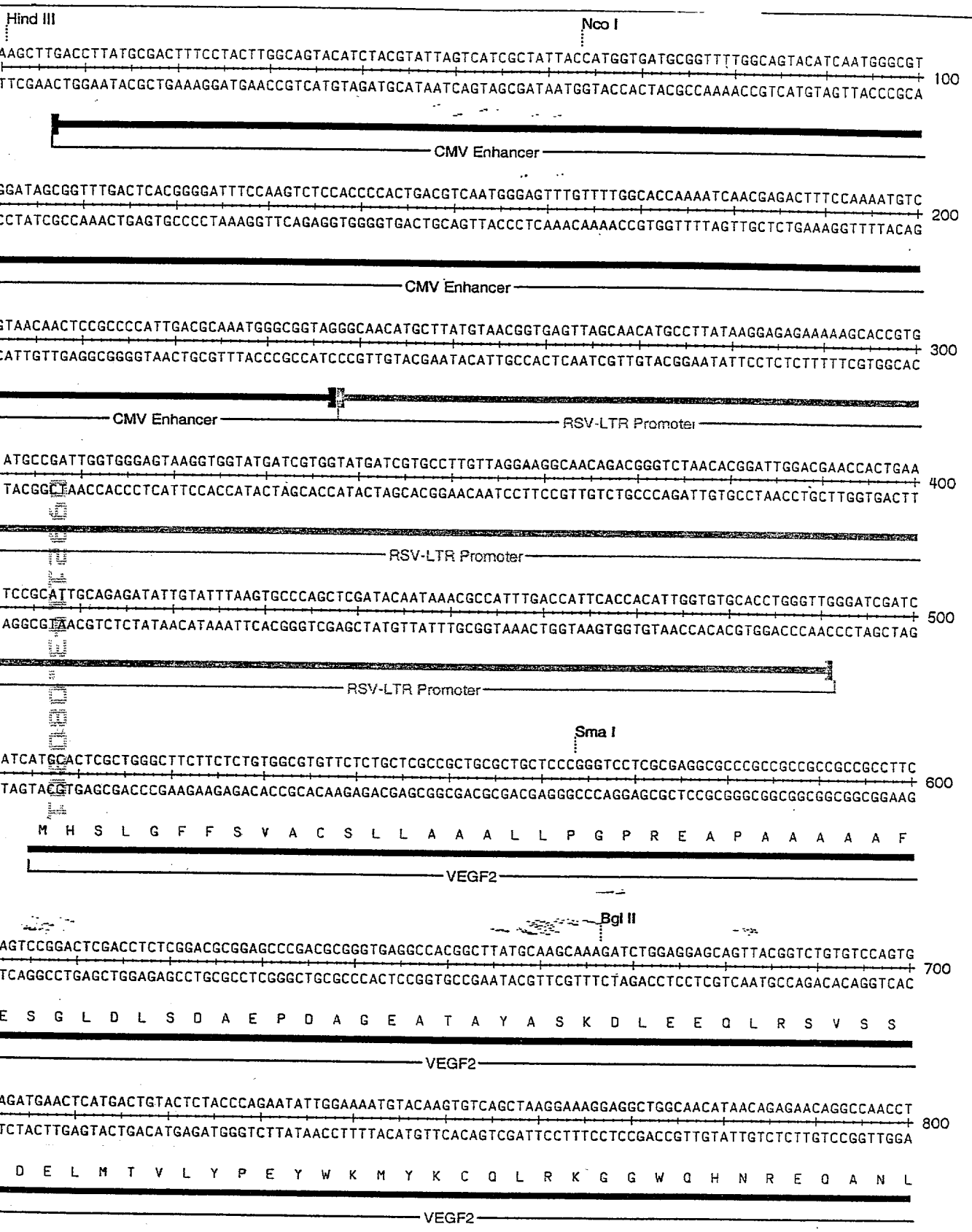

Hind III
Nco I
AAGCTTGACCTTATGCGACTTTCCTACTTGGCAGTACATCTACGTATTAGTCATCGCTATTACCATGGTGATGCGGTTTTGGCAGTACATCAATGGGCGT
TTCGAACTGGAATACGCTGAAAGGATGAACCGTCATGTAGATGCATAATCAGTAGCGATAATGGTACCACTACGCCAAAACCGTCATGTAGTTACCCGCA
100
CMV Enhancer
GGATAGCGGTTTGACTCACGGGGATTTCCAAGTCTCCACCCCACTGACGTCAATGGGAGTTTGTTTTGGCACCAAAATCAACGAGACTTTCCAAAATGTC
CCTATCGCCAAACTGAGTGCCCCTAAAGGTTCAGAGGTGGGGTGACTGCAGTTACCCTCAAACAAAACCGTGGTTTTAGTTGCTCTGAAAGGTTTTACAG
200
CMV Enhancer
GTAACAACTCCGCCCCATTGACGCAAATGGGCGGTAGGGCAACATGCTTATGTAACGGTGAGTTAGCAACATGCCTTATAAGGAGAGAAAAAGCACCGTG
CATTGTTGAGGCGGGGTAACTGCGTTTACCCGCCATCCCGTTGTACGAATACATTGCCACTCAATCGTTGTACGGAATATTCCTCTCTTTTTCGTGGCAC
300
CMV Enhancer
RSV-LTR Promoter
ATGCCGATTGGTGGGAGTAAGGTGGTATGATCGTGGTATGATCGTGCCTTGTTAGGAAGGCAACAGACGGGTCTAACACGGATTGGACGAACCACTGAA
TACGGCTAACCACCCTCATTCCACCATACTAGCACCATACTAGCACGGAACAATCCTTCCGTTGTCTGCCCAGATTGTGCCTAACCTGCTTGGTGACTT
400
RSV-LTR Promoter
TCCGCATTGCAGAGATATTGTATTTAAGTGCCCAGCTCGATACAATAAACGCCATTTGACCATTCACCACATTGGTGTGCACCTGGGTTGGGATCGATC
AGGCGTAACGTCTCTATAACATAAATTCACGGGTCGAGCTATGTTATTTGCGGTAAACTGGTAAGTGGTGTAACCACACGTGGACCCAACCCTAGCTAG
500
RSV-LTR Promoter
Sma I
ATCATGCACTCGCTGGGCTTCTTCTCTGTGGCGTGTTCTCTGCTCGCCGCTGCGCTGCTCCCGGGTCCTCGCGAGGCGCCCGCCGCCGCCGCCGCCTTC
TAGTACGTGAGCGACCCGAAGAAGAGACACCGCACAAGAGACGAGCGGCGACGCGACGAGGGCCCAGGAGCGCTCCGCGGGCGGCGGCGGCGGCGGAAG
600
M H S L G F F S V A C S L L A A A L L P G P R E A P A A A A A F
VEGF2
Bgl II
AGTCCGGACTCGACCTCTCGGACGCGGAGCCCGACGCGGGTGAGGCCACGGCTTATGCAAGCAAAGATCTGGAGGAGCAGTTACGGTCTGTGTCCAGTG
TCAGGCCTGAGCTGGAGAGCCTGCGCCTCGGGCTGCGCCCACTCCGGTGCCGAATACGTTCGTTTCTAGACCTCCTCGTCAATGCCAGACACAGGTCAC
700
E S G L D L S D A E P D A G E A T A Y A S K D L E E Q L R S V S S
VEGF2
AGATGAACTCATGACTGTACTCTACCCAGAATATTGGAAAATGTACAAGTGTCAGCTAAGGAAAGGAGGCTGGCAACATAACAGAGAACAGGCCAACCT
TCTACTTGAGTACTGACATGAGATGGGTCTTATAACCTTTTACATGTTCACAGTCGATTCCTTTCCTCCGACCGTTGTATTGTCTCTTGTCCGGTTGGA
800
D E L M T V L Y P E Y W K M Y K C Q L R K G G W Q H N R E Q A N L
VEGF2

FIG. 31B

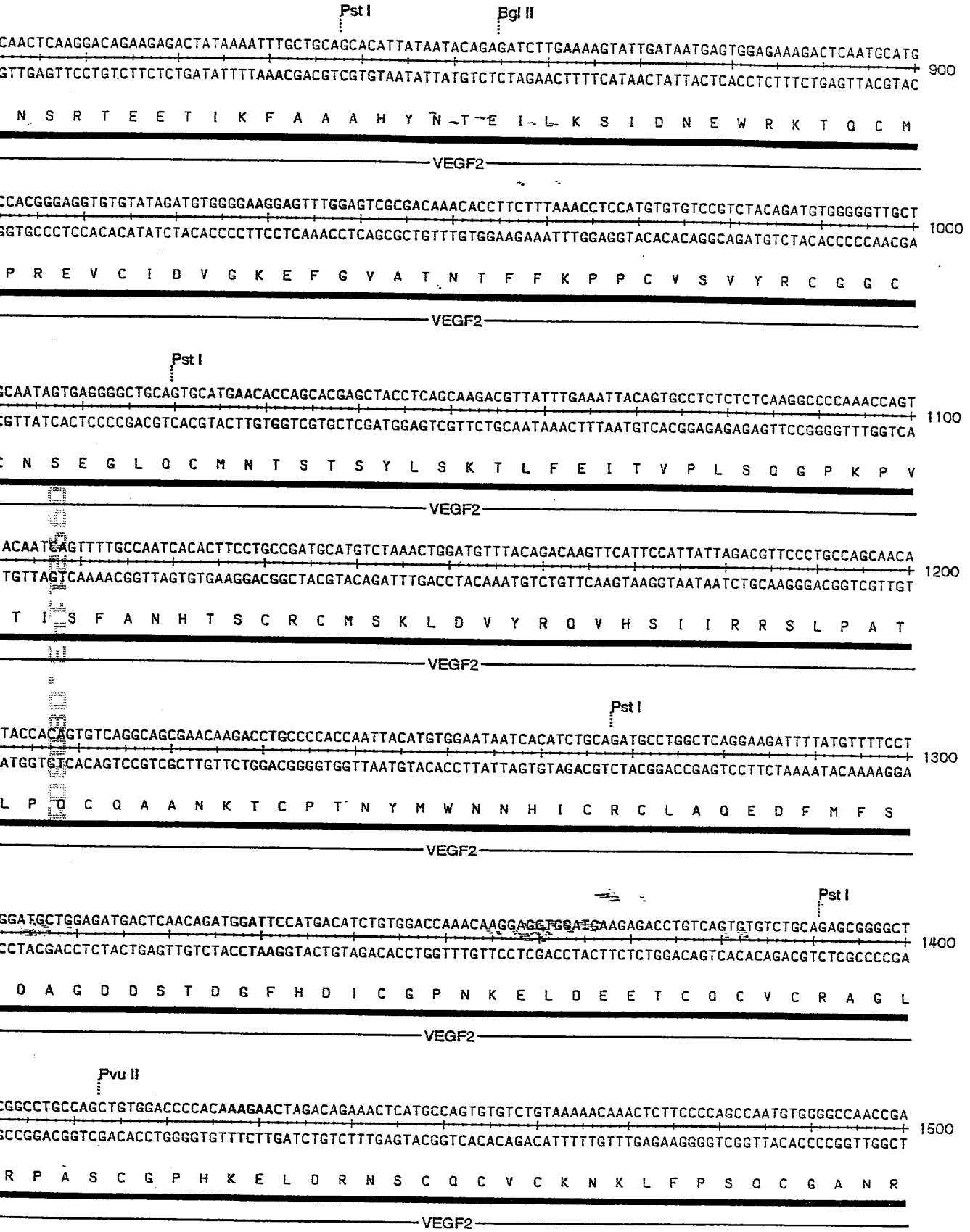
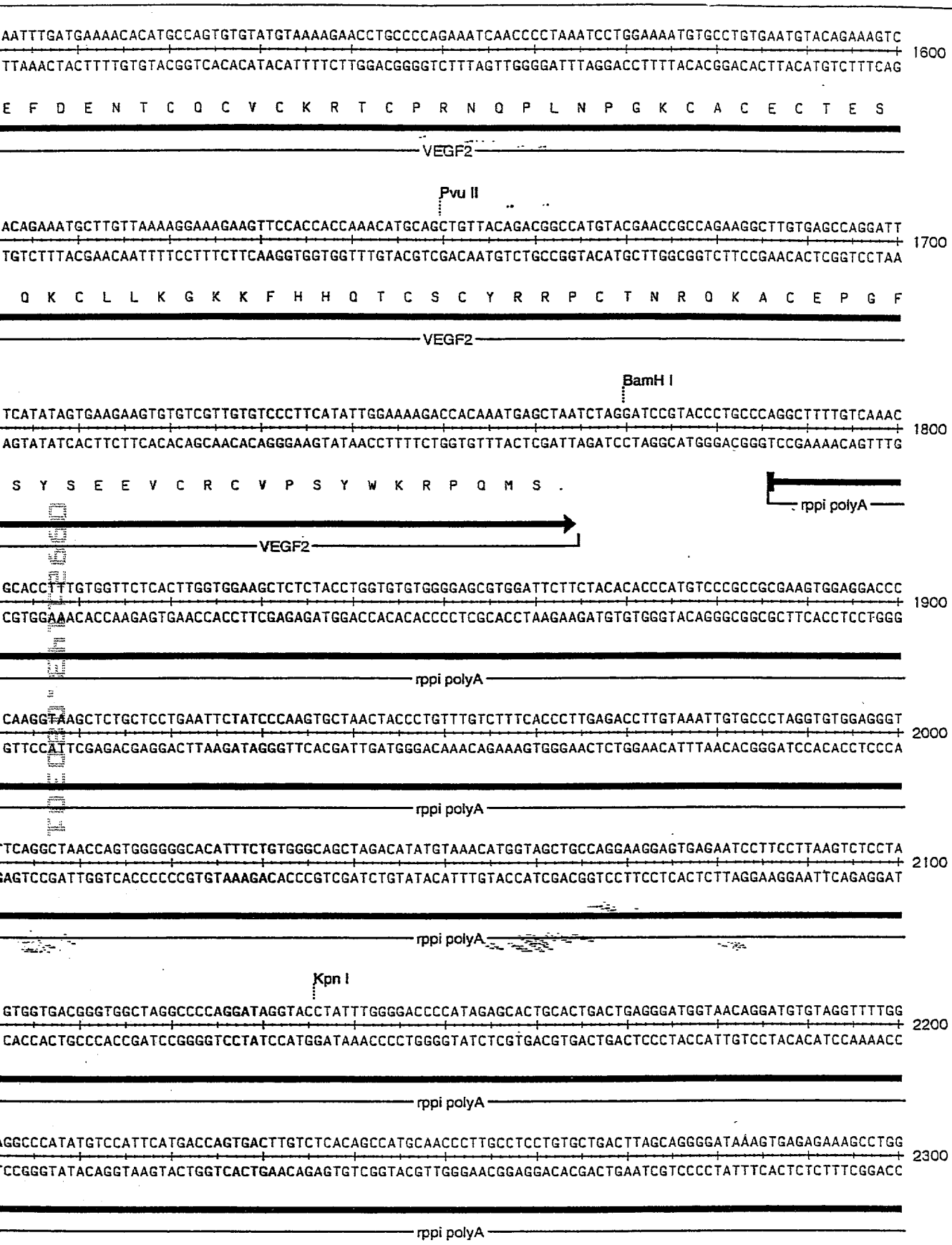

Pst I
Bgl II
CAACTCAAGGACAGAAGAGACTATAAAATTTGCTGCAGCACATTATAATACAGAGATCTTGAAAAGTATTGATAATGAGTGGAGAAAGACTCAATGCATG
GTTGAGTTCCTGTCTTCTCTGATATTTTAAACGACGTCGTGTAATATTATGTCTCTAGAACTTTTCATAACTATTACTCACCTCTTTCTGAGTTACGTAC
900
N S R T E E T I K F A A A H Y N T E I L K S I D N E W R K T Q C M
VEGF2
CCACGGGAGGTGTGTATAGATGTGGGGAAGGAGTTTGGAGTCGCGACAAACACCTTCTTTAAACCTCCATGTGTGTCCGTCTACAGATGTGGGGGTTGCT
GGTGCCCTCCACACATATCTACACCCCTTCCTCAAACCTCAGCGCTGTTTGTGGAAGAAATTTGGAGGTACACACAGGCAGATGTCTACACCCCCAACGA
1000
P R E V C I D V G K E F G V A T N T F F K P P C V S V Y R C G G C
VEGF2
Pst I
GCAATAGTGAGGGGCTGCAGTGCATGAACACCAGCACGAGCTACCTCAGCAAGACGTTATTTGAAATTACAGTGCCTCTCTCTCAAGGCCCCAAACCAGT
CGTTATCACTCCCCGACGTCACGTACTTGTGGTCGTGCTCGATGGAGTCGTTCTGCAATAAACTTTAATGTCACGGAGAGAGAGTTCCGGGGTTTGGTCA
1100
C N S E G L Q C M N T S T S Y L S K T L F E I T V P L S Q G P K P V
VEGF2
ACAATCAGTTTTGCCAATCACACTTCCTGCCGATGCATGTCTAAACTGGATGTTTACAGACAAGTTCATTCCATTATTAGACGTTCCCTGCCAGCAACA
TGTTAGTCAAAACGGTTAGTGTGAAGGACGGCTACGTACAGATTTGACCTACAAATGTCTGTTCAAGTAAGGTAATAATCTGCAAGGGACGGTCGTTGT
1200
T I S F A N H T S C R C M S K L D V Y R Q V H S I I R R S L P A T
VEGF2
Pst I
TACCACAGTGTCAGGCAGCGAACAAGACCTGCCCCACCAATTACATGTGGAATAATCACATCTGCAGATGCCTGGCTCAGGAAGATTTTATGTTTTCCT
ATGGTGTCACAGTCCGTCGCTTGTTCTGGACGGGGTGGTTAATGTACACCTTATTAGTGTAGACGTCTACGGACCGAGTCCTTCTAAAATACAAAAGGA
1300
L P Q C Q A A N K T C P T N Y M W N N H I C R C L A Q E D F M F S
VEGF2
Pst I
GGATGCTGGAGATGACTCAACAGATGGATTCCATGACATCTGTGGACCAAACAAGGAGCTGGATGAAGAGACCTGTCAGTGTGTCTGCAGAGCGGGGCT
CCTACGACCTCTACTGAGTTGTCTACCTAAGGTACTGTAGACACCTGGTTTGTTCCTCGACCTACTTCTCTGGACAGTCACACAGACGTCTCGCCCCGA
1400
D A G D D S T D G F H D I C G P N K E L D E E T C Q C V C R A G L
VEGF2
Pvu II
CGGCCTGCCAGCTGTGGACCCCACAAAGAACTAGACAGAAACTCATGCCAGTGTGTCTGTAAAAACAAACTCTTCCCCAGCCAATGTGGGGCCAACCGA
GCCGGACGGTCGACACCTGGGGTGTTTCTTGATCTGTCTTTGAGTACGGTCACACAGACATTTTTGTTTGAGAAGGGGTCGGTTACACCCCGGTTGGCT
1500
R P A S C G P H K E L D R N S C Q C V C K N K L F P S Q C G A N R
VEGF2

FIG. 31C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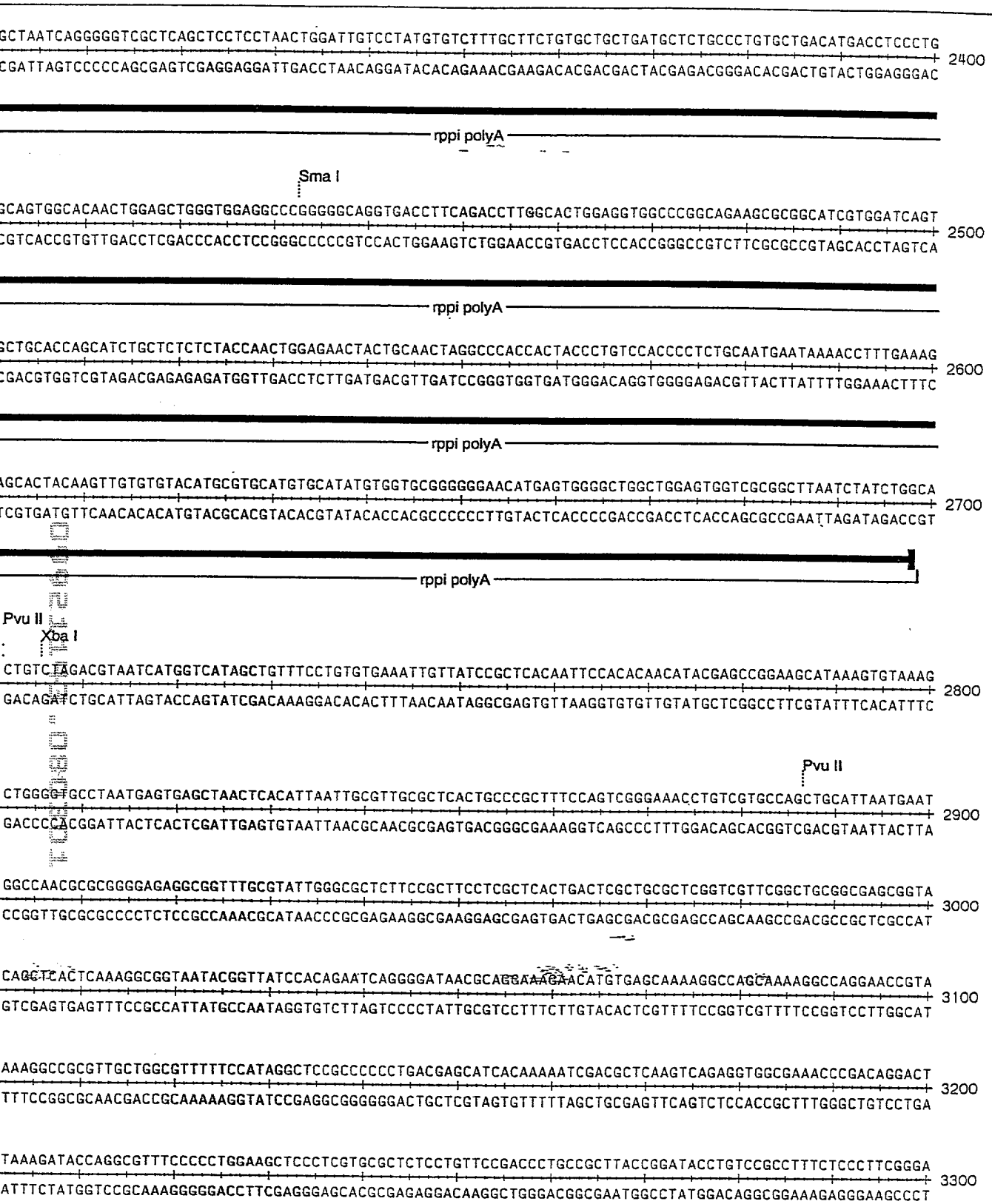
TTAAACTACTTTTGTGTACGGTCACACATACATTTTCTTGGACGGGGTCTTTAGTTGGGGATTTAGGACCTTTTACACGGACACTTACATGTCTTTCAG
1600
E F D E N T C Q C V C K R T C P R N Q P L N P G K C A C E C T E S
VEGF2
Pvu II
ACAGAAATGCTTGTTAAAAGGAAAGAAGTTCCACCACCAAACATGCAGCTGTTACAGACGGCCATGTACGAACCGCCAGAAGGCTTGTGAGCCAGGATT
TGTCTTTACGAACAATTTTCCTTTCTTCAAGGTGGTGGTTTGTACGTCGACAATGTCTGCCGGTACATGCTTGGCGGTCTTCCGAACACTCGGTCCTAA
1700
Q K C L L K G K K F H H Q T C S C Y R R P C T N R Q K A C E P G F
VEGF2
BamH I
TCATATAGTGAAGAAGTGTGTCGTTGTGTCCCTTCATATTGGAAAAGACCACAAATGAGCTAATCTAGGATCCGTACCCTGCCCAGGCTTTTGTCAAAC
AGTATATCACTTCTTCACACAGCAACACAGGGAAGTATAACCTTTTCTGGTGTTTACTCGATTAGATCCTAGGCATGGGACGGGTCCGAAAACAGTTTG
1800
S Y S E E V C R C V P S Y W K R P Q M S .
rppi polyA
VEGF2
GCACCTTTGTGGTTCTCACTTGGTGGAAGCTCTCTACCTGGTGTGTGGGGAGCGTGGATTCTTCTACACACCCATGTCCCGCCGCGAAGTGGAGGACCC
CGTGGAAACACCAAGAGTGAACCACCTTCGAGAGATGGACCACACACCCCTCGCACCTAAGAAGATGTGTGGGTACAGGGCGGCGCTTCACCTCCTGGG
1900
rppi polyA
CAAGGTAAGCTCTGCTCCTGAATTCTATCCCAAGTGCTAACTACCCTGTTTGTCTTTCACCCTTGAGACCTTGTAAATTGTGCCCTAGGTGTGGAGGGT
GTTCCATTCGAGACGAGGACTTAAGATAGGGTTCACGATTGATGGGACAAACAGAAAGTGGGAACTCTGGAACATTTAACACGGGATCCACACCTCCCA
2000
rppi polyA
TCAGGCTAACCAGTGGGGGGCACATTTCTGTGGGCAGCTAGACATATGTAAACATGGTAGCTGCCAGGAAGGAGTGAGAATCCTTCCTTAAGTCTCCTA
GAGTCCGATTGGTCACCCCCCGTGTAAAGACACCCGTCGATCTGTATACATTTGTACCATCGACGGTCCTTCCTCACTCTTAGGAAGGAATTCAGAGGAT
2100
rppi polyA
Kpn I
GTGGTGACGGGTGGCTAGGCCCCAGGATAGGTACCTATTTGGGGACCCCATAGAGCACTGCACTGACTGAGGGATGGTAACAGGATGTGTAGGTTTTGG
CACCACTGCCCACCGATCCGGGGTCCTATCCATGGATAAACCCCTGGGGTATCTCGTGACGTGACTGACTCCCTACCATTGTCCTACACATCCAAAACC
2200
rppi polyA
AGGCCCATATGTCCATTCATGACCAGTGACTTGTCTCACAGCCATGCAACCCTTGCCTCCTGTGCTGACTTAGCAGGGGATAAAGTGAGAGAAAGCCTGG
TCCGGGTATACAGGTAAGTACTGGTCACTGAACAGAGTGTCGGTACGTTGGGAACGGAGGACACGACTGAATCGTCCCCTATTTCACTCTCTTTCGGACC
2300
rppi polyA

FIG. 31D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2400
rppi polyA
Sma I
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2500
rppi polyA
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2600
rppi polyA
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2700
rppi polyA
Pvu II
Xba I
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GACAGATCTGCATTAGTACCAGTATCGACAAAGGACACACTTTAACAATAGGCGAGTGTTAAGGTGTGTTGTATGCTCGGCCTTCGTATTTCACATTTC
2800
Pvu II
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GACCCCACGGATTACTCACTCGATTGAGTGTAATTAACGCAACGCGAGTGACGGGCGAAAGGTCAGCCCTTTGGACAGCACGGTCGACGTAATTACTTA
2900
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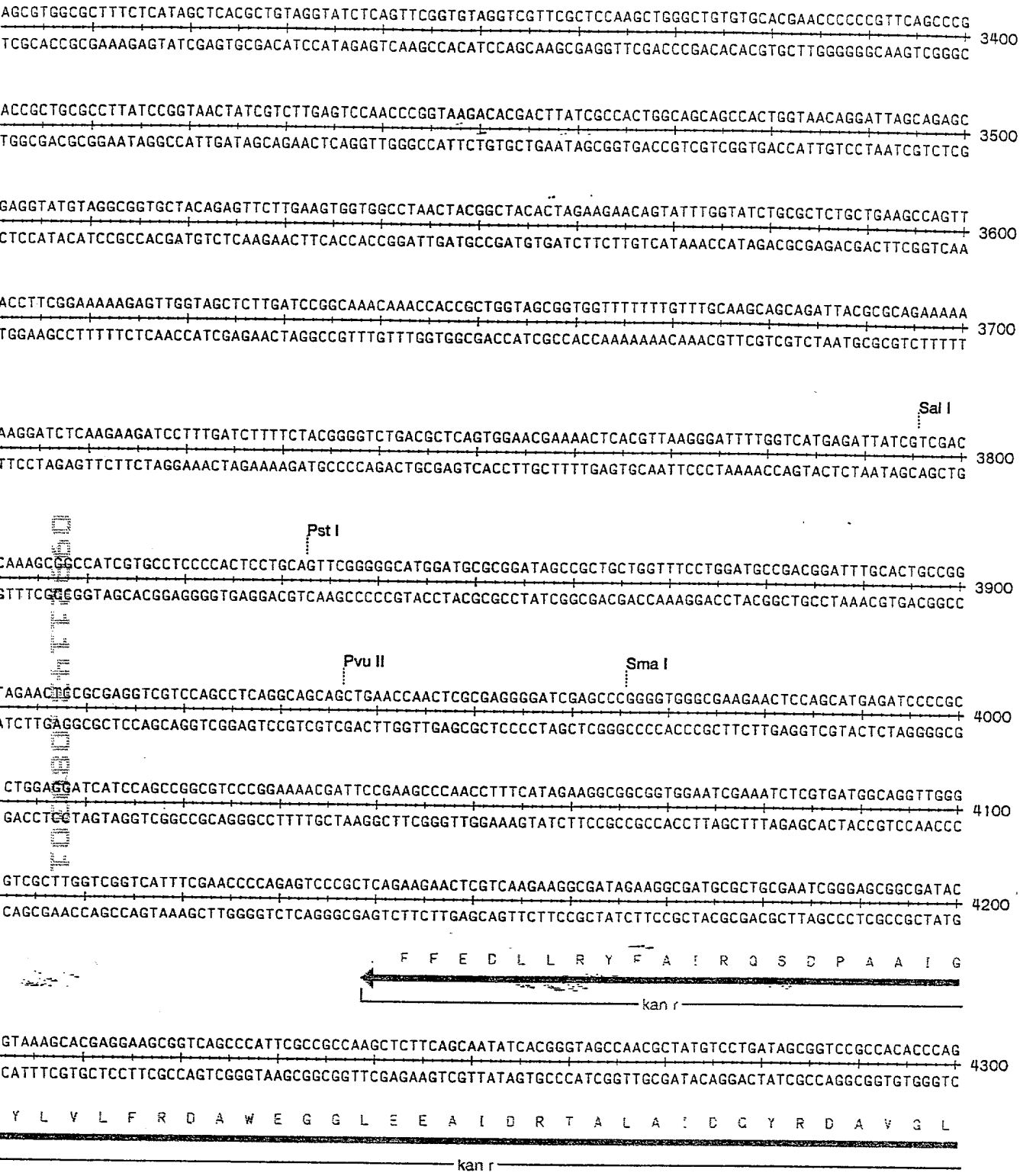
CCGGTTGCGCGCCCCTCTCCGCCAAACGCATAACCCGCGAGAAGGCGAAGGAGCGAGTGACTGAGCGACGCGAGCCAGCAAGCCGACGCCGCTCGCCAT
3000
CAGGTCACTCAAAGGCGGTAATACGGTTATCCACAGAATCAGGGGATAACGCAGGAAAGAACATGTGAGCAAAAGGCCAGCAAAAGGCCAGGAACCGTA
GTCGAGTGAGTTTCCGCCATTATGCCAATAGGTGTCTTAGTCCCCTATTGCGTCCTTTCTTGTACACTCGTTTTCCGGTCGTTTTCCGGTCCTTGGCAT
3100
AAAGGCCGCGTTGCTGGCGTTTTTCCATAGGCTCCGCCCCCCTGACGAGCATCACAAAAATCGACGCTCAAGTCAGAGGTGGCGAAACCCGACAGGACT
TTTCCGGCGCAACGACCGCAAAAAGGTATCCGAGGCGGGGGGACTGCTCGTAGTGTTTTTAGCTGCGAGTTCAGTCTCCACCGCTTTGGGCTGTCCTGA
3200
TAAAGATACCAGGCGTTTCCCCCTGGAAGCTCCCTCGTGCGCTCTCCTGTTCCGACCCTGCCGCTTACCGGATACCTGTCCGCCTTTCTCCCTTCGGGA
ATTTCTATGGTCCGCAAAGGGGGACCTTCGAGGGAGCACGCGAGAGGACAAGGCTGGGACGGCGAATGGCCTATGGACAGGCGGAAAGAGGGAAGCCCT
3300

FIG. 31E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TCGCACCGCGAAAGAGTATCGAGTGCGACATCCATAGAGTCAAGCCACATCCAGCAAGCGAGGTTCGACCCGACACACGTGCTTGGGGGGCAAGTCGGGC
3400
ACCGCTGCGCCTTATCCGGTAACTATCGTCTTGAGTCCAACCCGGTAAGACACGACTTATCGCCACTGGCAGCAGCCACTGGTAACAGGATTAGCAGAGC
TGGCGACGCGGAATAGGCCATTGATAGCAGAACTCAGGTTGGGCCATTCTGTGCTGAATAGCGGTGACCGTCGTCGGTGACCATTGTCCTAATCGTCTCG
3500
GAGGTATGTAGGCGGTGCTACAGAGTTCTTGAAGTGGTGGCCTAACTACGGCTACACTAGAAGAACAGTATTTGGTATCTGCGCTCTGCTGAAGCCAGTT
CTCCATACATCCGCCACGATGTCTCAAGAACTTCACCACCGGATTGATGCCGATGTGATCTTCTTGTCATAAACCATAGACGCGAGACGACTTCGGTCAA
3600
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TGGAAGCCTTTTTCTCAACCATCGAGAACTAGGCCGTTTGTTTGGTGGCGACCATCGCCACCAAAAAAACAAACGTTCGTCGTCTAATGCGCGTCTTTTT
3700
Sal I
AAGGATCTCAAGAAGATCCTTTGATCTTTTCTACGGGGTCTGACGCTCAGTGGAACGAAAACTCACGTTAAGGGATTTTGGTCATGAGATTATCGTCGAC
TTCCTAGAGTTCTTCTAGGAAACTAGAAAAGATGCCCCAGACTGCGAGTCACCTTGCTTTTGAGTGCAATTCCCTAAAACCAGTACTCTAATAGCAGCTG
3800
Pst I
CAAAGCGGCCATCGTGCCTCCCCACTCCTGCAGTTCGGGGGCATGGATGCGCGGATAGCCGCTGCTGGTTTCCTGGATGCCGACGGATTTGCACTGCCGG
GTTTCGCCGGTAGCACGGAGGGGTGAGGACGTCAAGCCCCCGTACCTACGCGCCTATCGGCGACGACCAAAGGACCTACGGCTGCCTAAACGTGACGGCC
3900
Pvu II
Sma I
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ATCTTGAGGCGCTCCAGCAGGTCGGAGTCCGTCGTCGACTTGGTTGAGCGCTCCCCTAGCTCGGGCCCCACCCGCTTCTTGAGGTCGTACTCTAGGGGCG
4000
CTGGAGGATCATCCAGCCGGCGTCCCGGAAAACGATTCCGAAGCCCAACCTTTCATAGAAGGCGGCGGTGGAATCGAAATCTCGTGATGGCAGGTTGGG
GACCTCCTAGTAGGTCGGCCGCAGGGCCTTTTGCTAAGGCTTCGGGTTGGAAAGTATCTTCCGCCGCCACCTTAGCTTTAGAGCACTACCGTCCAACCC
4100
GTCGCTTGGTCGGTCATTTCGAACCCCAGAGTCCCGCTCAGAAGAACTCGTCAAGAAGGCGATAGAAGGCGATGCGCTGCGAATCGGGAGCGGCGATAC
CAGCGAACCAGCCAGTAAAGCTTGGGGTCTCAGGGCGAGTCTTCTTGAGCAGTTCTTCCGCTATCTTCCGCTACGCGACGCTTAGCCCTCGCCGCTATG
4200
F F E D L L R Y F A I R Q S D P A A I G
kan r
GTAAAGCACGAGGAAGCGGTCAGCCCATTCGCCGCCAAGCTCTTCAGCAATATCACGGGTAGCCAACGCTATGTCCTGATAGCGGTCCGCCACACCCAG
CATTTCGTGCTCCTTCGCCAGTCGGGTAAGCGGCGGTTCGAGAAGTCGTTATAGTGCCCATCGGTTGCGATACAGGACTATCGCCAGGCGGTGTGGGTC
4300
Y L V L F R D A W E G G L E E A I D R T A L A I D C Y R D A V G L
kan r

FIG. 31F

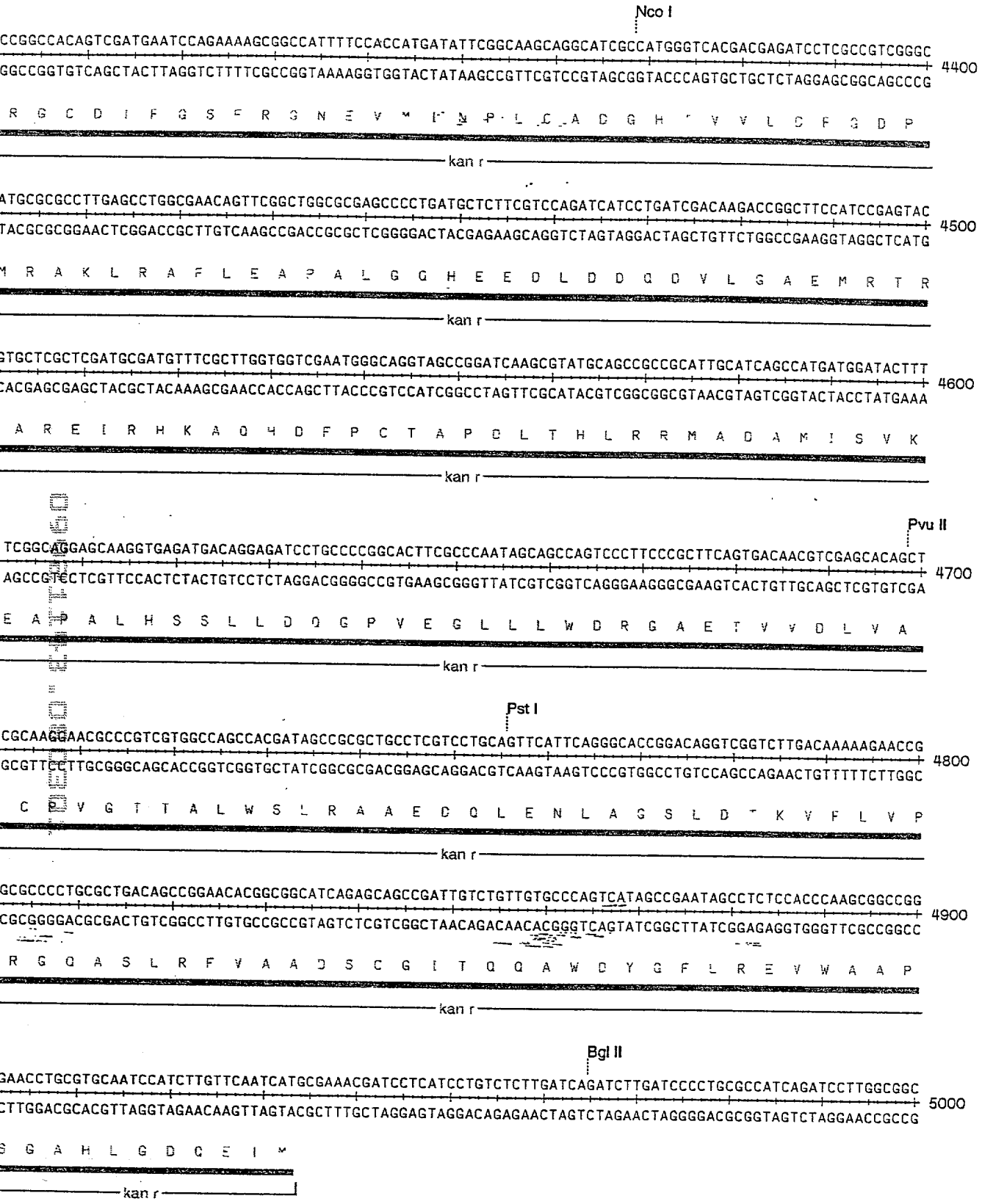
Nco I
4400
kan r
4500
kan r
4600
kan r
Pvu II
4700
kan r
Pst I
4800
kan r
4900
kan r
Bgl II
5000
kan r

FIG. 31G

Pvu II

```
AAGAAAGCCATCCAGTTTACTTTGCAGGGCTTCCCAACCTTACCAGAGGGCGCCCCAGCTGGCAATTCCGGTTCGCTTGCTGTCCATAAAACCGCCCAGT
                                                                                                     5100
TTCTTTCGGTAGGTCAAATGAAACGTCCCGAAGGGTTGGAATGGTCTCCCGCGGGGTCGACCGTTAAGGCCAAGCGAACGACAGGTATTTTGGCGGGTCA

CTAGCTATCGCCATGTAAGCCCACTGCAAGCTACCTGCTTTCTCTTTGCGCTTGCGTTTTCCCTTGTCCAGATAGCCCAGTAGCTGACATTCATCCGGGG
                                                                                                     5200
GATCGATAGCGGTACATTCGGGTGACGTTCGATGGACGAAAGAGAAACGCGAACGCAAAAGGGAACAGGTCTATCGGGTCATCGACTGTAAGTAGGCCCC

TCAGCACCGTTTCTGCGGACTGGCTTTCTACGTGTTCCGCTTCCTTTAGCAGCCCTTGCGCCCTGAGTGCTTGCGGCAGCGTG
                                                                                     5283
AGTCGTGGCAAAGACGCCTGACCGAAAGATGCACAAGGCGAAGGAAATCGTCGGGAACGCGGGACTCACGAACGCCGTCGCAC
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